STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 127446

TO: Terra Gibbs **Location:** **Art Unit: 1635** **July 16, 2004** **Case Serial Number: 10/024369**	**From: P. Sheppard** **Location: Remsen Building** **Phone: (571) 272-2529** **sheppard@uspto.gov**

2C18

Search Notes

7/15/04

Schreiber, David

From: Gibbs, Terra
Sent: Monday, June 28, 2004 10:57 AM
To: Schreiber, David
Subject: Sequence search request...

Hi David,
I have another request for a score over length search:
I need a length limited nucleotide sequence search of SEQ ID NO:47 in USSN 10/024,369,
NOTE: SEQ ID NO:47 is a 20-mer
where the returns are rank ordered based on the score over length/ratio as we've discussed. I need the lengths limited to hits between 8 and 50 nucleotides, and I'll take as many hits as you can import into excel (64,000?), and alignments for anything above .75 on the above ratio. Hope this is clear, please call me if it's not. I also need the interference databases searched if possible.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
571-272-0758

OM nucleic - nucleic search, using sw model

Run on: July 15, 2004, 18:07:01 ; Search time 0.001 Seconds
(without alignments)
0.320 Million cell updates/sec

Title: us-10-024-369-47
Perfect score: 20
Sequence: 1 cccaccttcttgggcagaag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 8 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2000 summaries

Database : estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query % Match	Length	DB	ID	Description
c	1	6	30.0	8	1	CA851350	ACCESSION:CA851350
	2	4	20.0	8	1	CA851350	ACCESSION:CA851350

ALIGNMENTS

RESULT 1
CA851350/c
LOCUS CA851350 8 bp mRNA linear EST 01-AUG-2003
DEFINITION D12G08_N20_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D12G08 5', mRNA sequence.
ACCESSION CA851350
VERSION CA851350.1 GI:33388143
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 8)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
FEATURES Location/Qualifiers
source 1. .8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D12G08"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          8 TCTTGGG 14
              | |||||
Db          8 TNTTGGG 2
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RESULT 2
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LOCUS CA851350 8 bp mRNA linear EST 01-AUG-2003
DEFINITION D12G08_N20_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D12G08 5', mRNA sequence.
ACCESSION CA851350
VERSION CA851350.1 GI:33388143
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 8)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
FEATURES Location/Qualifiers
source 1. .8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D12G08"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCA 4
              ||||
Db          2 CCCA 5
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Search completed: July 15, 2004, 18:07:02

Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 15, 2004, 16:39:00 ; Search time 0.001 Seconds
(without alignments)
32.440 Million cell updates/sec

Title: us-10-024-369-47
Perfect score: 20
Sequence: 1 cccaccttcttgggcagaag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 77 seqs, 811 residues

Total number of hits satisfying chosen parameters: 154

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2000 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	12	60.0	15	1	BD061440	ACCESSION:BD061440
	2	10	50.0	11	1	AX623364	ACCESSION:AX623364
	3	10	50.0	11	1	AX630785	ACCESSION:AX630785
c	4	9.4	47.0	11	1	AX472203	ACCESSION:AX472203
c	5	9	45.0	10	1	BD238992	ACCESSION:BD238992
c	6	9	45.0	10	1	BD239512	ACCESSION:BD239512
c	7	9	45.0	10	1	BD239813	ACCESSION:BD239813
	8	9	45.0	11	1	AR353840	ACCESSION:AR353840
	9	9	45.0	11	1	AX625163	ACCESSION:AX625163
	10	9	45.0	11	1	AX632584	ACCESSION:AX632584
	11	9	45.0	12	1	AR349259	ACCESSION:AR349259
	12	9	45.0	12	1	AR349261	ACCESSION:AR349261
c	13	8.4	42.0	10	1	A92569	ACCESSION:A92569
c	14	8.4	42.0	10	1	AR043677	ACCESSION:AR043677
	15	8.4	42.0	10	1	BD238844	ACCESSION:BD238844
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c	20	8.4	42.0	10	1	AX301616	ACCESSION:AX301616
	21	8.4	42.0	10	1	AX374630	ACCESSION:AX374630
c	22	8.4	42.0	10	1	AX805907	ACCESSION:AX805907
	23	8.4	42.0	10	1	BD161343	ACCESSION:BD161343
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c	26	8.4	42.0	11	1	AR081174	ACCESSION:AR081174
c	27	8.4	42.0	11	1	AR085371	ACCESSION:AR085371
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c	32	8.4	42.0	11	1	AR171617	ACCESSION:AR171617
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	38	8.4	42.0	11	1	AX471682	ACCESSION:AX471682
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	85	5.4	27.0	10	1	AX152798	ACCESSION:AX152798
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	96	5	25.0	9	1	AX668814	ACCESSION:AX668814
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144	4	20.0	11	1	AX626126	ACCESSION:AX626126
145	4	20.0	11	1	AX627751	ACCESSION:AX627751
c 146	4	20.0	11	1	AX627837	ACCESSION:AX627837
147	4	20.0	11	1	AX630798	ACCESSION:AX630798
c 148	3.8	19.0	10	1	AR303500	ACCESSION:AR303500
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152	3.4	17.0	11	1	AX625581	ACCESSION:AX625581
c 153	3.4	17.0	11	1	AX628191	ACCESSION:AX628191
154	3.4	17.0	11	1	AX630930	ACCESSION:AX630930

ALIGNMENTS

```
RESULT 1
BD061440
LOCUS       BD061440                  15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for selectively separating living cell expressed with
            specific gene.
ACCESSION   BD061440
VERSION     BD061440.1  GI:22607046
KEYWORDS    JP 2001286285-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ishibashi,K. and Tsuji,A.
  TITLE     Method for selectively separating living cell expressed with
            specific gene
  JOURNAL   Patent: JP 2001286285-A 2 16-OCT-2001;
            LABORATORY OF MOLECULAR BIOPHOTONICS
COMMENT     OS   Artificial Sequence
            PN   JP 2001286285-A/2
            PD   16-OCT-2001
            PF   28-APR-2000 JP 2000130793
            PI   KANAME ISHIBASHI,AKIHIKO TSUJI
            PC   C12N15/09,C12N1/02,C12N5/10,C12Q1/68,G01N33/48,G01N33/53, PC
            G01N33/566,
            PC   G01N33/58//(C12N1/02,C12R1:91),(C12Q1/68,C12R1:91),C12N15/00,
            PC   C12N5/00
            CC   Probe
            FH   Key             Location/Qualifiers.
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     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             60.0%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTGGGCA 16
              ||||||||||||
Db          3 CCTTCTTGGGCA 14


RESULT 2
AX623364
LOCUS       AX623364                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 405 from Patent WO02053774.
ACCESSION   AX623364
VERSION     AX623364.1  GI:28451305
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 405 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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Qy          5 CCTTCTTGGG 14
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Db          1 CCTTCTTGGG 10


RESULT 3
AX630785
LOCUS       AX630785                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7826 from Patent WO02053774.
ACCESSION   AX630785
VERSION     AX630785.1  GI:28458825
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7826 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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Qy          5 CCTTCTTGGG 14
              ||||||||||
Db          1 CCTTCTTGGG 10


RESULT 4
AX472203/c
LOCUS       AX472203                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 194 from Patent WO02053775.
ACCESSION   AX472203
VERSION     AX472203.1  GI:22207240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 194 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES             Location/Qualifiers
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  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 12;
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Qy          8 TCTTGGGCAGA 18
              |||| ||||||
Db         11 TCTTTGGCAGA 1


RESULT 5
BD238992/c
LOCUS       BD238992                 10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238992
VERSION     BD238992.1  GI:33048762
KEYWORDS    JP 2002534056-A/410.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 410 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/410
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db          9 CCCACCTTC 1


RESULT 6
BD239512/c
LOCUS       BD239512                 10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239512
VERSION     BD239512.1  GI:33049282
KEYWORDS    JP 2002534056-A/930.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 930 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/930
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
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            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
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            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
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            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
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           FH   Key             Location/Qualifiers
           FT   source          1. .10
           FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
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                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGGCAGAA 19
               |||||||||
Db          10 TGGGCAGAA 2


RESULT 7
BD239813/c
LOCUS       BD239813                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239813
VERSION     BD239813.1  GI:33049583
KEYWORDS    JP 2002534056-A/1231.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1231 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1231
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
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            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
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            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 CCACCTTCT 10
               |||||||||
Db          10 CCACCTTCT 2


RESULT 8
AR353840
LOCUS       AR353840                  11 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6593111.
ACCESSION   AR353840
VERSION     AR353840.1  GI:33759907
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Baric,R.S. and Yount,B.
  TITLE     Directional assembly of large viral genomes and chromosomes
  JOURNAL   Patent: US 6593111-A 15 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           5 CCTTCTTGG 13
               |||||||||
Db           2 CCTTCTTGG 10


RESULT 9
AX625163
LOCUS       AX625163                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2204 from Patent WO02053774.
ACCESSION   AX625163
VERSION     AX625163.1  GI:28453104
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2204 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 GGGCAGAAG 20
               |||||||||
Db           1 GGGCAGAAG 9


RESULT 10
AX632584
LOCUS       AX632584                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9626 from Patent WO02053774.
ACCESSION   AX632584
VERSION     AX632584.1  GI:28468199
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9626 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAAG 20
              |||||||||
Db          1 GGGCAGAAG 9


RESULT 11
AR349259
LOCUS       AR349259                  12 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6583986.
ACCESSION   AR349259
VERSION     AR349259.1  GI:33749984
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Storti,W.J., Sibley,K., Ovadia,S., Kimball,S. and Falvo,B.
  TITLE     Method and apparatus for managing thermal energy emissions
  JOURNAL   Patent: US 6583986-A 6 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGC 15
              |||||||||
Db          2 TTCTTGGGC 10


RESULT 12
AR349261
LOCUS       AR349261                  12 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6583986.
ACCESSION   AR349261
VERSION     AR349261.1  GI:33749986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Storti,W.J., Sibley,K., Ovadia,S., Kimball,S. and Falvo,B.
  TITLE     Method and apparatus for managing thermal energy emissions
  JOURNAL   Patent: US 6583986-A 8 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGC 15
              |||||||||
Db          2 TTCTTGGGC 10


RESULT 13
A92569/c
LOCUS       A92569                    10 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 10 from Patent WO9812320.
ACCESSION   A92569
VERSION     A92569.1  GI:6741228
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Stoecklin,E. and Groner,B.
  TITLE     NUCLEIC ACID CONSTRUCT CODING FOR A PROTEIN COMPLEX FROM A STAT
            PROTEIN AND A NUCLEAR RECEPTOR AND ITS USE
  JOURNAL   Patent: WO 9812320-A 10 26-MAR-1998;
            STOECKLIN ELISABETH (CH); GRONER BERND (CH)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              ||||||||| |
Db         10 TTCTTGGGAA 1


RESULT 14
AR043677/c
LOCUS       AR043677                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 47 from patent US 5814517.
ACCESSION   AR043677
VERSION     AR043677.1  GI:5964685
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 47 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              ||||||||| |
Db         10 TTCTTGGGAA 1


RESULT 15
BD238844
LOCUS       BD238844                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238844
VERSION     BD238844.1  GI:33048614
KEYWORDS    JP 2002534056-A/262.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 262 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/262
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
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            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              | ||||||||
Db          1 TGCTTGGGCA 10


RESULT 16
BD239019
LOCUS       BD239019                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239019
VERSION     BD239019.1  GI:33048789
KEYWORDS    JP 2002534056-A/437.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 437 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/437
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
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            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
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            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||||| |||
Db          1 CCACCTGCTT 10


RESULT 17
BD240663/c
LOCUS       BD240663                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240663
VERSION     BD240663.1  GI:33050433
KEYWORDS    JP 2002534056-A/2081.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 2081 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/2081
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
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            08-DEC-1998 US    60/111715
            PI    BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC    C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC    C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC    C12N15/00,C12N5/00,C12N15/00
            CC    Preparation and use of superior vaccines
            FH    Key             Location/Qualifiers
            FT    source          1. .10
            FT                    /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              |||||| |||
Db         10 CCCACCCTCT 1


RESULT 18
AR303500
LOCUS       AR303500                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 225 from patent US 6544736.
ACCESSION   AR303500
VERSION     AR303500.1  GI:31692276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 225 08-APR-2003;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TCTTGGGCAG 17
              ||||| ||||
Db          1 TCTTGAGCAG 10


RESULT 19
AX152798/c
LOCUS       AX152798                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 713 from Patent WO0138577.
ACCESSION   AX152798
VERSION     AX152798.1  GI:14534449
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 713 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 20
AX301616/c
LOCUS       AX301616                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 330 from Patent WO0185941.
ACCESSION   AX301616
VERSION     AX301616.1  GI:17382699
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 330 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 21
AX374630
LOCUS       AX374630                  10 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 51 from Patent WO0210454.
ACCESSION   AX374630
VERSION     AX374630.1  GI:19169527
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Choi,J.Y., Koshy,B., Kliem,S. and Stephens,J.C.
  TITLE     Haplotypes of the alas2 gene
  JOURNAL   Patent: WO 0210454-A 51 07-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              | ||||||||
Db          1 CATCTTGGGC 10
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RESULT 22
AX805907/c
LOCUS       AX805907                  10 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 53 from Patent WO03060163.
ACCESSION   AX805907
VERSION     AX805907.1  GI:38522818
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Eijk,M.J. and van Schaik,C.
  TITLE     Discrimination and detection of target nucleotide sequences using
            mass spectrometry
  JOURNAL   Patent: WO 03060163-A 53 24-JUL-2003;
            Keygene N.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stuffer sequence"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              |||||| |||
Db         10 CCCACCCTCT 1


RESULT 23
BD161343
LOCUS       BD161343                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161343
VERSION     BD161343.1  GI:27867101
KEYWORDS    JP 2002186482-A/165.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 165 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/165
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              |||| |||||
Db          1 TTGGCCAGAA 10


RESULT 24
BD166511/c
LOCUS       BD166511                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166511
VERSION     BD166511.1  GI:27872323
KEYWORDS    JP 2002209591-A/56.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 56 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/56
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 25
AR074494/c
LOCUS       AR074494                  11 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 73 from patent US 5955075.
ACCESSION   AR074494
VERSION     AR074494.1  GI:10001249
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Method of inhibiting tumor growth using antibodies to MN protein
  JOURNAL   Patent: US 5955075-A 73 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1
```

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RESULT 26
AR081174/c
LOCUS       AR081174                  11 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 73 from patent US 5972353.
ACCESSION   AR081174
VERSION     AR081174.1  GI:10007902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
  JOURNAL   Patent: US 5972353-A 73 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 27
AR085371/c
LOCUS       AR085371                  11 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 73 from patent US 5981711.
ACCESSION   AR085371
VERSION     AR085371.1  GI:10012140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN-specific antibodies and hybridomas
  JOURNAL   Patent: US 5981711-A 73 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 28
AR088119/c
LOCUS       AR088119                  11 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 73 from patent US 5989838.
ACCESSION   AR088119
VERSION     AR088119.1  GI:10014882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Immunological methods of detecting MN proteins and MN polypeptides
  JOURNAL   Patent: US 5989838-A 73 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 29
AR104278/c
LOCUS       AR104278                  11 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 73 from patent US 6093548.
ACCESSION   AR104278
VERSION     AR104278.1  GI:12816986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Detection and quantitation of MN-specific antibodies
  JOURNAL   Patent: US 6093548-A 73 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 30
AR143540/c
LOCUS       AR143540                  11 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 73 from patent US 6204370.
ACCESSION   AR143540
VERSION     AR143540.1  GI:15104826
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6204370-A 73 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 31
AR171446/c
LOCUS       AR171446                  11 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 73 from patent US 6297041.
ACCESSION   AR171446
VERSION     AR171446.1  GI:17910396
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297041-A 73 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 32
AR171617/c
LOCUS       AR171617                  11 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 73 from patent US 6297051.
ACCESSION   AR171617
VERSION     AR171617.1  GI:17910567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297051-A 73 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 33
BD243207/c
LOCUS       BD243207                  11 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  MN gene and protein.
ACCESSION   BD243207
VERSION     BD243207.1  GI:33052977
KEYWORDS    JP 2002528085-A/56.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: JP 2002528085-A 56 03-SEP-2002;
            INSTITUTE OF VIROLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002528085-A/56
            PD   03-SEP-2002
            PF   22-OCT-1999 JP 2000578465
            PR   23-OCT-1998 US    09/177776,23-OCT-1998 US    09/178115 PI
            JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC
            C07K14/47,
            PC   C12Q1/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
            CC   MN gene and protein
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 34
I34822/c
LOCUS       I34822                    11 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 15 from patent US 5599673.
ACCESSION   I34822
VERSION     I34822.1  GI:2087790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Keating,M.T., Curran,M.E. and Wang,Q.
  TITLE     Long QT syndrome genes
  JOURNAL   Patent: US 5599673-A 15 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTCCT 1


RESULT 35
AX412934
LOCUS       AX412934                  11 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 698 from Patent WO0222675.
ACCESSION   AX412934
VERSION     AX412934.1  GI:21445392
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
  TITLE     Plant genes, the expression of which are altered by pathogen
            infection
  JOURNAL   Patent: WO 0222675-A 698 21-MAR-2002;
            Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
            CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
            Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:3702"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              ||||||| ||
Db          2 TTGGGCAAAA 11


RESULT 36
AX470593/c
LOCUS       AX470593                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 170 from Patent WO02053773.
ACCESSION   AX470593
VERSION     AX470593.1  GI:22205718
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 170 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||| |||||
Db         11 CCACTTTCTT 2


RESULT 37
AX471678
LOCUS       AX471678                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1255 from Patent WO02053773.
ACCESSION   AX471678
VERSION     AX471678.1  GI:22206803
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1255 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              |||||||| |
Db          2 CACCTTCTGG 11


RESULT 38
AX471682
LOCUS       AX471682                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1259 from Patent WO02053773.
ACCESSION   AX471682
VERSION     AX471682.1  GI:22206807
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1259 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              |||||| |||
Db          2 CACCTTATTG 11


RESULT 39
AX623377/c
LOCUS       AX623377                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 418 from Patent WO02053774.
ACCESSION   AX623377
VERSION     AX623377.1  GI:28451318
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 418 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              ||| ||||||
Db         11 CACTTTCTTG 2


RESULT 40
AX623396
LOCUS       AX623396                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 437 from Patent WO02053774.
ACCESSION   AX623396
VERSION     AX623396.1  GI:28451337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

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REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 437 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||| ||||||
Db          2 CCCGCCTTCT 11


RESULT 41
AX623509/c
LOCUS       AX623509                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 550 from Patent WO02053774.
ACCESSION   AX623509
VERSION     AX623509.1  GI:28451450
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 550 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||||| |||
Db         10 CCACCTCCTT 1


RESULT 42
AX625581/c
LOCUS       AX625581                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2622 from Patent WO02053774.
ACCESSION   AX625581
VERSION     AX625581.1  GI:28453522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2622 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              ||||||| ||
Db         10 CCACCTTTTT 1


RESULT 43
AX626059
LOCUS       AX626059                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3100 from Patent WO02053774.
ACCESSION   AX626059
VERSION     AX626059.1  GI:28454097
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3100 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||| ||||
Db          2 CCCACTTTCT 11


RESULT 44
AX626126/c
LOCUS       AX626126                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3167 from Patent WO02053774.
ACCESSION   AX626126
VERSION     AX626126.1  GI:28454164
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3167 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              |||||| |||
Db         10 CCCACCCTCT 1


RESULT 45
AX626949
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LOCUS       AX626949                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3990 from Patent WO02053774.
ACCESSION   AX626949
VERSION     AX626949.1  GI:28454987
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3990 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              ||||||||| |
Db          1 TTGGGCAGGA 10


RESULT 46
AX627089/c
LOCUS       AX627089                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4130 from Patent WO02053774.
ACCESSION   AX627089
VERSION     AX627089.1  GI:28455127
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4130 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              || |||||||
Db         11 TTTTTGGGCA 2


RESULT 47
AX627751/c
LOCUS       AX627751                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4792 from Patent WO02053774.
ACCESSION   AX627751
VERSION     AX627751.1  GI:28455789
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4792 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||| |||||
Db         11 CCACTTTCTT 2


RESULT 48
AX627792
LOCUS       AX627792                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4833 from Patent WO02053774.
ACCESSION   AX627792
VERSION     AX627792.1  GI:28455830
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4833 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              |||||||| |
Db          2 CACCTTCTGG 11


RESULT 49
AX627837
LOCUS       AX627837                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4878 from Patent WO02053774.
ACCESSION   AX627837
VERSION     AX627837.1  GI:28455875
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4878 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
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  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||||| |||
Db          1 CCACCTGCTT 10


RESULT 50
AX628191
LOCUS       AX628191                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5232 from Patent WO02053774.
ACCESSION   AX628191
VERSION     AX628191.1  GI:28456229
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5232 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              |||||| |||
Db          2 CACCTTATTG 11


RESULT 51
AX628263
LOCUS       AX628263                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5304 from Patent WO02053774.
ACCESSION   AX628263
VERSION     AX628263.1  GI:28456301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5304 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              ||||| ||||
Db          2 TTGGGTAGAA 11


RESULT 52
AX629947/c
LOCUS       AX629947                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6988 from Patent WO02053774.
ACCESSION   AX629947
VERSION     AX629947.1  GI:28457985
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6988 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 53
AX630798/c
LOCUS       AX630798                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7839 from Patent WO02053774.
ACCESSION   AX630798
VERSION     AX630798.1  GI:28458838
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7839 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              ||| ||||||
Db         11 CACTTTCTTG 2


RESULT 54
AX630817
LOCUS       AX630817                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7858 from Patent WO02053774.
ACCESSION   AX630817
VERSION     AX630817.1  GI:28458857
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7858 11-JUL-2002;
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            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||| ||||||
Db          2 CCCGCCTTCT 11


RESULT 55
AX630930/c
LOCUS       AX630930                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7971 from Patent WO02053774.
ACCESSION   AX630930
VERSION     AX630930.1  GI:28458972
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7971 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||||| |||
Db         10 CCACCTCCTT 1


RESULT 56
AX632853
LOCUS       AX632853                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9895 from Patent WO02053774.
ACCESSION   AX632853
VERSION     AX632853.1  GI:28468468
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9895 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CTTGGGCAGA 18
              |||||||| |
Db          2 CTTGGGCACA 11


RESULT 57
AX480947
LOCUS       AX480947                   9 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 7 from Patent WO0246412.
ACCESSION   AX480947
VERSION     AX480947.1  GI:22217586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rebar,E., Jamieson,A., Liu,Q., Liu,P.Q., Wolffe,A., Eisenberg,S.P.
            and Jarvis,E.
  TITLE     Regulation of angiogenesis with zinc finger proteins
  JOURNAL   Patent: WO 0246412-A 7 13-JUN-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="target"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGCAGA 18
              ||||||||
Db          1 TGGGCAGA 8


RESULT 58
AX668629/c
LOCUS       AX668629                   9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2078 from Patent WO0242459.
ACCESSION   AX668629
VERSION     AX668629.1  GI:29291602
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2078 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          8 CCCACCTT 1


RESULT 59
AX668630/c
LOCUS       AX668630                   9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2079 from Patent WO0242459.
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ACCESSION   AX668630
VERSION     AX668630.1  GI:29291603
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2079 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          8 CCCACCTT 1


RESULT 60
AX668813/c
LOCUS       AX668813                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2262 from Patent WO0242459.
ACCESSION   AX668813
VERSION     AX668813.1  GI:29291788
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2262 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db          9 CACCTTCT 2


RESULT 61
AX668814/c
LOCUS       AX668814                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2263 from Patent WO0242459.
ACCESSION   AX668814
VERSION     AX668814.1  GI:29291789
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2263 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db          9 CACCTTCT 2


RESULT 62
AB012724
LOCUS       AB012724                  9 bp    DNA     linear   PRI 30-JUN-1998
DEFINITION  Homo sapiens gene for endothelin-A receptor, cis_element region.
ACCESSION   AB012724
VERSION     AB012724.1  GI:3273319
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hosoda,K., Nakao,K., Tamura,N., Arai,H., Ogawa,Y., Suga,S.,
            Nakanishi,S. and Imura,H.
  TITLE     Organization, structure, chromosomal assignment, and expression of
            the gene encoding the human endothelin-A receptor
  JOURNAL   J. Biol. Chem. 267 (26), 18797-18804 (1992)
  MEDLINE   92406798
   PUBMED   1326535
REFERENCE   2  (sites)
  AUTHORS   Yamashita,J., Yoshimasa,T., Arai,H., Hiraoka,J., Takaya,K.,
            Miyamoto,Y., Ogawa,Y., Itoh,H. and Nakao,K.
  TITLE     Identification of cis-elements of the human endothelin-A receptor
            gene and inhibition of the gene expression by the decoy strategy
  JOURNAL   J. Biol. Chem. 273 (26), 15993-15999 (1998)
  MEDLINE   98298101
   PUBMED   9632648
REFERENCE   3  (bases 1 to 9)
  AUTHORS   Yamashita,J., Yoshimasa,T., Arai,H., Itoh,H. and Nakao,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1998) Jun Yamashita, Kyoto University Graduate
            School of Medicine, Department of Medicine and Clinical Science; 54
            Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan
            (E-mail:juny@kuhp.kyoto-u.ac.jp, Tel:81-75-751-3170,
            Fax:81-75-771-9452)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    1. .9
                     /note="cis_element of the human endothelin-A receptor
                     gene"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          2 CCCACCTT 9


RESULT 63
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A15662
LOCUS       A15662                    10 bp    DNA     linear   PAT 10-FEB-1994
DEFINITION  oligonucleotide.
ACCESSION   A15662
VERSION     A15662.1  GI:489794
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Verrips,C.T., Ledeboer,A.M., Edens,L., Klok,R. and Maat,J.
  TITLE     DNA sequences encoding various allelic forms of mature thaumatin,
            recombinant plasmids comprising said DNA's and a process for their
            preparation, bacterial cultures comprising said recombinant
            plasmids, and method for producing mature thaumatin
  JOURNAL   Patent: EP 0054330-A 4 23-JUN-1982;
            UNILEVER NV; UNILEVER PLC
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db          2 CCACCTTC 9


RESULT 64
BD238780
LOCUS       BD238780                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238780
VERSION     BD238780.1  GI:33048550
KEYWORDS    JP 2002534056-A/198.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 198 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/198
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 GGGCAGAA 19
               ||||||||
Db           1 GGGCAGAA 8


RESULT 65
BD238878
LOCUS       BD238878                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238878
VERSION     BD238878.1  GI:33048648
KEYWORDS    JP 2002534056-A/296.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 296 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/296
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          3 CACCTTCT 10
              ||||||||
Db          2 CACCTTCT 9


RESULT 66
BD238880
LOCUS       BD238880                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238880
VERSION     BD238880.1  GI:33048650
KEYWORDS    JP 2002534056-A/298.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 298 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/298
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          3 CCCACCTT 10


RESULT 67
BD239283/c
LOCUS       BD239283                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239283
VERSION     BD239283.1  GI:33049053
KEYWORDS    JP 2002534056-A/701.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 701 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/701
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
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            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
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            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
              ||||||||
Db          9 GGCAGAAG 2


RESULT 68
BD239952
LOCUS       BD239952                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239952
VERSION     BD239952.1  GI:33049722
KEYWORDS    JP 2002534056-A/1370.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1370 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1370
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
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            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GGCAGAAG 20
               ||||||||
Db           1 GGCAGAAG 8


RESULT 69
BD240374
LOCUS       BD240374                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240374
VERSION     BD240374.1  GI:33050144
KEYWORDS    JP 2002534056-A/1792.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1792 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1792
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           5 CCTTCTTG 12
               ||||||||
Db           1 CCTTCTTG 8


RESULT 70
BD240388/c
LOCUS       BD240388                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240388
VERSION     BD240388.1  GI:33050158
KEYWORDS    JP 2002534056-A/1806.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1806 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1806
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
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            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GGCAGAAG 20
               ||||||||
Db           9 GGCAGAAG 2


RESULT 71
BD240561/c
LOCUS       BD240561                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240561
VERSION     BD240561.1  GI:33050331
KEYWORDS    JP 2002534056-A/1979.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1979 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1979
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
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            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db          9 CCACCTTC 2


RESULT 72
I19168/c
LOCUS       I19168                    10 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 31 from patent US 5502176.
ACCESSION   I19168
VERSION     I19168.1  GI:1599523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Tenen,D.G., Pahl,H.L. and Burn,T.C.
  TITLE     Myeloid cell specific promoter
  JOURNAL   Patent: US 5502176-A 31 26-MAR-1996;
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GGCAGAAG 20
               ||||||||
Db           8 GGCAGAAG 1


RESULT 73
I19170/c
LOCUS       I19170                    10 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 33 from patent US 5502176.
ACCESSION   I19170
VERSION     I19170.1  GI:1599525
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Tenen,D.G., Pahl,H.L. and Burn,T.C.
  TITLE     Myeloid cell specific promoter
  JOURNAL   Patent: US 5502176-A 33 26-MAR-1996;
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 GGGCAGAA 19
               ||||||||
Db          10 GGGCAGAA 3


RESULT 74
AR303345/c
LOCUS       AR303345                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 70 from patent US 6544736.
ACCESSION   AR303345
VERSION     AR303345.1  GI:31692121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 70 08-APR-2003;
FEATURES            Location/Qualifiers
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     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAA 19
              ||||||||
Db         10 GGGCAGAA 3


RESULT 75
AX152217
LOCUS       AX152217                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 132 from Patent WO0138577.
ACCESSION   AX152217
VERSION     AX152217.1  GI:14533868
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 132 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTG 12
              ||||||||
Db          1 CCTTCTTG 8


RESULT 76
AX153242/c
LOCUS       AX153242                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1157 from Patent WO0138577.
ACCESSION   AX153242
VERSION     AX153242.1  GI:14534893
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1157 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db         10 CACCTTCT 3


RESULT 77
AX301610/c
LOCUS       AX301610                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 324 from Patent WO0185941.
ACCESSION   AX301610
VERSION     AX301610.1  GI:17382693
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 324 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
              ||||||||
Db          9 GGCAGAAG 2


RESULT 78
BD238878/c
LOCUS       BD238878                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238878
VERSION     BD238878.1  GI:33048648
KEYWORDS    JP 2002534056-A/296.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 296 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/296
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
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            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
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            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
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            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
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            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 6;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 CAGAAG 20
               ||||||
Db          10 CAGAAG 5


RESULT 79
BD240388
LOCUS       BD240388                 10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240388
VERSION     BD240388.1  GI:33050158
KEYWORDS    JP 2002534056-A/1806.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1806 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1806
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 6;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCT 10
              ||||||
Db          1 CCTTCT 6


RESULT 80
AX153242
LOCUS       AX153242                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1157 from Patent WO0138577.
ACCESSION   AX153242
VERSION     AX153242.1  GI:14534893
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1157 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 6;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 CAGAAG 20
               ||||||
Db           2 CAGAAG 7


RESULT 81
AX625163/c
LOCUS       AX625163                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2204 from Patent WO02053774.
ACCESSION   AX625163
VERSION     AX625163.1  GI:28453104
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2204 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 6;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCT 10
              ||||||
Db         10 CCTTCT 5


RESULT 82
AX632584/c
LOCUS       AX632584                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9626 from Patent WO02053774.
```

```
ACCESSION   AX632584
VERSION     AX632584.1  GI:28468199
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9626 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 6;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCT 10
              ||||||
Db         10 CCTTCT 5


RESULT 83
AX471678/c
LOCUS       AX471678                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1255 from Patent WO02053773.
ACCESSION   AX471678
VERSION     AX471678.1  GI:22206803
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1255 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 6;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CAGAAG 20
              ||||||
Db         10 CAGAAG 5


RESULT 84
AX627792/c
LOCUS       AX627792                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4833 from Patent WO02053774.
ACCESSION   AX627792
VERSION     AX627792.1  GI:28455830
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4833 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 6;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CAGAAG 20
              ||||||
Db         10 CAGAAG 5


RESULT 85
AX152798
LOCUS       AX152798                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 713 from Patent WO0138577.
ACCESSION   AX152798
VERSION     AX152798.1  GI:14534449
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 713 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.0%;  Score 5.4;  DB 1;  Length 10;
  Best Local Similarity   85.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
              ||| |||
Db          1 GCACAAG 7


RESULT 86
AX301616
LOCUS       AX301616                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 330 from Patent WO0185941.
ACCESSION   AX301616
VERSION     AX301616.1  GI:17382699
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 330 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.0%;  Score 5.4;  DB 1;  Length 10;
  Best Local Similarity   85.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          14 GCAGAAG 20
               ||| |||
Db           1 GCACAAG 7


RESULT 87
BD166511
LOCUS       BD166511                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166511
VERSION     BD166511.1  GI:27872323
KEYWORDS    JP 2002209591-A/56.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 56 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/56
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             27.0%;  Score 5.4;  DB 1;  Length 10;
  Best Local Similarity   85.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          14 GCAGAAG 20
               ||| |||
Db           1 GCACAAG 7


RESULT 88
BD239952/c
LOCUS       BD239952                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239952
VERSION     BD239952.1  GI:33049722
KEYWORDS    JP 2002534056-A/1370.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1370 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1370
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             27.0%;  Score 5.4;  DB 1;  Length 10;
  Best Local Similarity   85.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           4 ACCTTCT 10
               | |||||
Db          10 ATCTTCT 4


RESULT 89
AX629947
LOCUS       AX629947                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6988 from Patent WO02053774.
ACCESSION   AX629947
VERSION     AX629947.1  GI:28457985
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6988 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.0%;  Score 5.4;  DB 1;  Length 11;
  Best Local Similarity   85.7%;  Pred. No. 94;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          14 GCAGAAG 20
               ||| |||
Db           1 GCACAAG 7


RESULT 90
AX626949/c
LOCUS       AX626949                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3990 from Patent WO02053774.
ACCESSION   AX626949
VERSION     AX626949.1  GI:28454987
KEYWORDS    .
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```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3990 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             26.0%;  Score 5.2;  DB 1;  Length 11;
  Best Local Similarity   70.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              ||| ||  ||
Db         11 TTCCTGCCCA 2


RESULT 91
AX627089
LOCUS       AX627089                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4130 from Patent WO02053774.
ACCESSION   AX627089
VERSION     AX627089.1  GI:28455127
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4130 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             26.0%;  Score 5.2;  DB 1;  Length 11;
  Best Local Similarity   70.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              |||  || ||
Db          1 TTGCCCAAAA 10


RESULT 92
AX632853/c
LOCUS       AX632853                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9895 from Patent WO02053774.
ACCESSION   AX632853
VERSION     AX632853.1  GI:28468468
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9895 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             26.0%;  Score 5.2;  DB 1;  Length 11;
  Best Local Similarity   70.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 TGGGCAGAAG 20
              || ||  |||
Db         11 TGTGCCCAAG 2


RESULT 93
AX668629
LOCUS       AX668629                 9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2078 from Patent WO0242459.
ACCESSION   AX668629
VERSION     AX668629.1  GI:29291602
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2078 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGC 15
              |||||
Db          5 TGGGC 9


RESULT 94
AX668630
LOCUS       AX668630                 9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2079 from Patent WO0242459.
ACCESSION   AX668630
VERSION     AX668630.1  GI:29291603
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2079 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGC 15
```

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              |||||
Db          5 TGGGC 9


RESULT 95
AX668813
LOCUS       AX668813                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2262 from Patent WO0242459.
ACCESSION   AX668813
VERSION     AX668813.1  GI:29291788
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2262 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAAG 20
              |||||
Db          2 AGAAG 6


RESULT 96
AX668814
LOCUS       AX668814                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2263 from Patent WO0242459.
ACCESSION   AX668814
VERSION     AX668814.1  GI:29291789
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2263 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAAG 20
              |||||
Db          2 AGAAG 6


RESULT 97
BD239813
LOCUS       BD239813                 10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239813
VERSION     BD239813.1  GI:33049583
KEYWORDS    JP 2002534056-A/1231.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1231 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1231
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAAG 20
              |||||
Db          2 AGAAG 6


RESULT 98
BD239283
LOCUS       BD239283                 10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239283
VERSION     BD239283.1  GI:33049053
KEYWORDS    JP 2002534056-A/701.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 701 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/701
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            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CTTCT 10
              |||||
Db          2 CTTCT 6


RESULT 99
BD240374/c
LOCUS       BD240374                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240374
VERSION     BD240374.1  GI:33050144
KEYWORDS    JP 2002534056-A/1792.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1792 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1792
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
                |||||
Db          6 AGAAG 2


RESULT 100
I19168
LOCUS       I19168                    10 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 31 from patent US 5502176.
ACCESSION   I19168
VERSION     I19168.1  GI:1599523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Tenen,D.G., Pahl,H.L. and Burn,T.C.
  TITLE     Myeloid cell specific promoter
  JOURNAL   Patent: US 5502176-A 31 26-MAR-1996;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CTTCT 10
              |||||
Db          1 CTTCT 5


RESULT 101
AX152217/c
LOCUS       AX152217                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 132 from Patent WO0138577.
ACCESSION   AX152217
VERSION     AX152217.1  GI:14533868
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 132 31-MAY-2001;
            The Johns Hopkins University (US)
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FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               |||||
Db           6 AGAAG 2


RESULT 102
AX301610
LOCUS       AX301610                10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 324 from Patent WO0185941.
ACCESSION   AX301610
VERSION     AX301610.1  GI:17382693
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 324 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           6 CTTCT 10
               |||||
Db           2 CTTCT 6


RESULT 103
AX623364/c
LOCUS       AX623364                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 405 from Patent WO02053774.
ACCESSION   AX623364
VERSION     AX623364.1  GI:28451305
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 405 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               |||||
Db           6 AGAAG 2


RESULT 104
AX630785/c
LOCUS       AX630785                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7826 from Patent WO02053774.
ACCESSION   AX630785
VERSION     AX630785.1  GI:28458825
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7826 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               |||||
Db           6 AGAAG 2


RESULT 105
AR353840/c
LOCUS       AR353840                11 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6593111.
ACCESSION   AR353840
VERSION     AR353840.1  GI:33759907
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Baric,R.S. and Yount,B.
  TITLE     Directional assembly of large viral genomes and chromosomes
  JOURNAL   Patent: US 6593111-A 15 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               |||||
Db           7 AGAAG 3


RESULT 106
AR074494
LOCUS       AR074494                11 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 73 from patent US 5955075.
ACCESSION   AR074494
VERSION     AR074494.1  GI:10001249
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Method of inhibiting tumor growth using antibodies to MN protein
  JOURNAL   Patent: US 5955075-A 73 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGC 15
              |||||
Db          7 TGGGC 11


RESULT 107
AR081174
LOCUS       AR081174                  11 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 73 from patent US 5972353.
ACCESSION   AR081174
VERSION     AR081174.1  GI:10007902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
  JOURNAL   Patent: US 5972353-A 73 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGC 15
              |||||
Db          7 TGGGC 11


RESULT 108
AR085371
LOCUS       AR085371                  11 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 73 from patent US 5981711.
ACCESSION   AR085371
VERSION     AR085371.1  GI:10012140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN-specific antibodies and hybridomas
  JOURNAL   Patent: US 5981711-A 73 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGC 15
              |||||
Db          7 TGGGC 11


RESULT 109
AR088119
LOCUS       AR088119                  11 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 73 from patent US 5989838.
ACCESSION   AR088119
VERSION     AR088119.1  GI:10014882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Immunological methods of detecting MN proteins and MN polypeptides
  JOURNAL   Patent: US 5989838-A 73 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGC 15
              |||||
Db          7 TGGGC 11


RESULT 110
AR104278
LOCUS       AR104278                  11 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 73 from patent US 6093548.
ACCESSION   AR104278
VERSION     AR104278.1  GI:12816986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Detection and quantitation of MN-specific antibodies
  JOURNAL   Patent: US 6093548-A 73 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGC 15
              ||||||
Db          7 TGGGC 11


RESULT 111
AR143540
LOCUS       AR143540                  11 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 73 from patent US 6204370.
ACCESSION   AR143540
VERSION     AR143540.1  GI:15104826
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6204370-A 73 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .11
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGGC 15
               |||||
Db           7 TGGGC 11


RESULT 112
AR171446
LOCUS       AR171446                  11 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 73 from patent US 6297041.
ACCESSION   AR171446
VERSION     AR171446.1  GI:17910396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297041-A 73 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGGC 15
               |||||
Db           7 TGGGC 11


RESULT 113
AR171617
LOCUS       AR171617                  11 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 73 from patent US 6297051.
ACCESSION   AR171617
VERSION     AR171617.1  GI:17910567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297051-A 73 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGGC 15
               |||||
Db           7 TGGGC 11


RESULT 114
BD243207
LOCUS       BD243207                  11 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  MN gene and protein.
ACCESSION   BD243207
VERSION     BD243207.1  GI:33052977
KEYWORDS    JP 2002528085-A/56.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: JP 2002528085-A 56 03-SEP-2002;
            INSTITUTE OF VIROLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002528085-A/56
            PD   03-SEP-2002
            PF   22-OCT-1999 JP 2000578465
            PR   23-OCT-1998 US    09/177776,23-OCT-1998 US    09/178115 PI
            JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC
            C07K14/47,
            PC   C12Q1/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
            CC   MN gene and protein
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGGC 15
               |||||
Db           7 TGGGC 11


RESULT 115
AX623396/c
LOCUS       AX623396                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 437 from Patent WO02053774.
ACCESSION   AX623396
VERSION     AX623396.1  GI:28451337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 437 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               |||||
Db          11 AGAAG 7


RESULT 116
AX630817/c
LOCUS       AX630817                  11 bp    DNA     linear   PAT 21-FEB-2003
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```
DEFINITION  Sequence 7858 from Patent WO02053774.
ACCESSION   AX630817
VERSION     AX630817.1  GI:28458857
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7858 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             25.0%;  Score 5;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAAG 20
              |||||
Db         11 AGAAG 7


RESULT 117
BD061440/c
LOCUS       BD061440                  15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for selectively separating living cell expressed with
            specific gene.
ACCESSION   BD061440
VERSION     BD061440.1  GI:22607046
KEYWORDS    JP 2001286285-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ishibashi,K. and Tsuji,A.
  TITLE     Method for selectively separating living cell expressed with
            specific gene
  JOURNAL   Patent: JP 2001286285-A 2 16-OCT-2001;
            LABORATORY OF MOLECULAR BIOPHOTONICS
COMMENT     OS   Artificial Sequence
            PN   JP 2001286285-A/2
            PD   16-OCT-2001
            PF   28-APR-2000 JP 2000130793
            PI   KANAME ISHIBASHI,AKIHIKO TSUJI
            PC   C12N15/09,C12N1/02,C12N5/10,C12Q1/68,G01N33/48,G01N33/53, PC
            G01N33/566,
            PC   G01N33/58//(C12N1/02,C12R1:91),(C12Q1/68,C12R1:91),C12N15/00,
            PC   C12N5/00
            CC   Probe
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             25.0%;  Score 5;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAAG 20
              |||||
Db          8 AGAAG 4


RESULT 118
AX412934/c
LOCUS       AX412934                  11 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 698 from Patent WO0222675.
ACCESSION   AX412934
VERSION     AX412934.1  GI:21445392
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
  TITLE     Plant genes, the expression of which are altered by pathogen
            infection
  JOURNAL   Patent: WO 0222675-A 698 21-MAR-2002;
            Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
            CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
            Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3702"

  Query Match             23.0%;  Score 4.6;  DB 1;  Length 11;
  Best Local Similarity   63.6%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 TCTTGGGCAGA 18
              | |||  || |
Db         11 TTTTGCCCAAA 1


RESULT 119
BD161343/c
LOCUS       BD161343                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161343
VERSION     BD161343.1  GI:27867101
KEYWORDS    JP 2002186482-A/165.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 165 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/165
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             22.0%;  Score 4.4;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTG 12
              |||| |
Db         10 TTCTGG 5
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RESULT 120
AX628263/c
LOCUS       AX628263                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5304 from Patent WO02053774.
ACCESSION   AX628263
VERSION     AX628263.1  GI:28456301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5304 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             22.0%;  Score 4.4;  DB 1;  Length 11;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACC 6
              |||| |
Db          6 CCCAAC 1


RESULT 121
AR349259/c
LOCUS       AR349259                  12 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6583986.
ACCESSION   AR349259
VERSION     AR349259.1  GI:33749984
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Storti,W.J., Sibley,K., Ovadia,S., Kimball,S. and Falvo,B.
  TITLE     Method and apparatus for managing thermal energy emissions
  JOURNAL   Patent: US 6583986-A 6 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAAG 20
              | ||  |||
Db         12 GAGCCCAAG 4


RESULT 122
AR349261/c
LOCUS       AR349261                  12 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6583986.
ACCESSION   AR349261
VERSION     AR349261.1  GI:33749986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Storti,W.J., Sibley,K., Ovadia,S., Kimball,S. and Falvo,B.
  TITLE     Method and apparatus for managing thermal energy emissions
  JOURNAL   Patent: US 6583986-A 8 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAAG 20
              | ||  |||
Db         12 GAGCCCAAG 4


RESULT 123
AX480947/c
LOCUS       AX480947                   9 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 7 from Patent WO0246412.
ACCESSION   AX480947
VERSION     AX480947.1  GI:22217586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rebar,E., Jamieson,A., Liu,Q., Liu,P.Q., Wolffe,A., Eisenberg,S.P.
            and Jarvis,E.
  TITLE     Regulation of angiogenesis with zinc finger proteins
  JOURNAL   Patent: WO 0246412-A 7 13-JUN-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="target"

  Query Match             20.0%;  Score 4;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCA 4
              ||||
Db          4 CCCA 1


RESULT 124
AB012724/c
LOCUS       AB012724                   9 bp    DNA     linear   PRI 30-JUN-1998
DEFINITION  Homo sapiens gene for endothelin-A receptor, cis_element region.
ACCESSION   AB012724
VERSION     AB012724.1  GI:3273319
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hosoda,K., Nakao,K., Tamura,N., Arai,H., Ogawa,Y., Suga,S.,
            Nakanishi,S. and Imura,H.
  TITLE     Organization, structure, chromosomal assignment, and expression of
            the gene encoding the human endothelin-A receptor
  JOURNAL   J. Biol. Chem. 267 (26), 18797-18804 (1992)
  MEDLINE   92406798
   PUBMED   1326535
REFERENCE   2  (sites)
  AUTHORS   Yamashita,J., Yoshimasa,T., Arai,H., Hiraoka,J., Takaya,K.,
            Miyamoto,Y., Ogawa,Y., Itoh,H. and Nakao,K.
  TITLE     Identification of cis-elements of the human endothelin-A receptor
            gene and inhibition of the gene expression by the decoy strategy
  JOURNAL   J. Biol. Chem. 273 (26), 15993-15999 (1998)
  MEDLINE   98298101
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   PUBMED   9632648
REFERENCE   3  (bases 1 to 9)
  AUTHORS   Yamashita,J., Yoshimasa,T., Arai,H., Itoh,H. and Nakao,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1998) Jun Yamashita, Kyoto University Graduate
            School of Medicine, Department of Medicine and Clinical Science; 54
            Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan
            (E-mail:juny@kuhp.kyoto-u.ac.jp, Tel:81-75-751-3170,
            Fax:81-75-771-9452)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    1. .9
                     /note="cis_element of the human endothelin-A receptor
                     gene"

  Query Match             20.0%;  Score 4;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGG 14
               ||||
Db          5 TGGG 2


RESULT 125
BD238992
LOCUS       BD238992                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238992
VERSION     BD238992.1  GI:33048762
KEYWORDS    JP 2002534056-A/410.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 410 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/410
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 GAAG 20
               ||||
Db          1 GAAG 4


RESULT 126
BD239512
LOCUS       BD239512                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239512
VERSION     BD239512.1  GI:33049282
KEYWORDS    JP 2002534056-A/930.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 930 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/930
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCT 10
               ||||
Db          2 TTCT 5
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RESULT 127
A92569
LOCUS       A92569                    10 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 10 from Patent WO9812320.
ACCESSION   A92569
VERSION     A92569.1  GI:6741228
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Stoecklin,E. and Groner,B.
  TITLE     NUCLEIC ACID CONSTRUCT CODING FOR A PROTEIN COMPLEX FROM A STAT
            PROTEIN AND A NUCLEAR RECEPTOR AND ITS USE
  JOURNAL   Patent: WO 9812320-A 10 26-MAR-1998;
            STOECKLIN ELISABETH (CH); GRONER BERND (CH)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCA 4
              ||||
Db          3 CCCA 6


RESULT 128
AR043677
LOCUS       AR043677                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 47 from patent US 5814517.
ACCESSION   AR043677
VERSION     AR043677.1  GI:5964685
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 47 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCA 4
              ||||
Db          3 CCCA 6


RESULT 129
BD238844/c
LOCUS       BD238844                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238844
VERSION     BD238844.1  GI:33048614
KEYWORDS    JP 2002534056-A/262.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 262 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/262
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCA 4
              ||||
Db          8 CCCA 5


RESULT 130
BD239019/c
LOCUS       BD239019                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239019
VERSION     BD239019.1  GI:33048789
KEYWORDS    JP 2002534056-A/437.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 437 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/437
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
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            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 GCAG 17
               ||||
Db           8 GCAG 5


RESULT 131
BD240663
LOCUS       BD240663                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240663
VERSION     BD240663.1  GI:33050433
KEYWORDS    JP 2002534056-A/2081.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 2081 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/2081
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGG 14
               ||||
Db           7 TGGG 10


RESULT 132
AX374630/c
LOCUS       AX374630                  10 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 51 from Patent WO0210454.
ACCESSION   AX374630
VERSION     AX374630.1  GI:19169527
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Choi,J.Y., Koshy,B., Kliem,S. and Stephens,J.C.
  TITLE     Haplotypes of the alas2 gene
  JOURNAL   Patent: WO 0210454-A 51 07-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 CCCA 4
               ||||
Db           9 CCCA 6


RESULT 133
AX805907
LOCUS       AX805907                  10 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 53 from Patent WO03060163.
ACCESSION   AX805907
VERSION     AX805907.1  GI:38522818
KEYWORDS    .
SOURCE      synthètic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Eijk,M.J. and van Schaik,C.
  TITLE     Discrimination and detection of target nucleotide sequences using
            mass spectrometry
  JOURNAL   Patent: WO 03060163-A 53 24-JUL-2003;
            Keygene N.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
                     /note="stuffer sequence"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGG 14
               ||||
Db           7 TGGG 10


RESULT 134
A15662/c
LOCUS       A15662                    10 bp    DNA     linear   PAT 10-FEB-1994
DEFINITION  oligonucleotide.
ACCESSION   A15662
VERSION     A15662.1  GI:489794
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Verrips,C.T., Ledeboer,A.M., Edens,L., Klok,R. and Maat,J.
  TITLE     DNA sequences encoding various allelic forms of mature thaumatin,
            recombinant plasmids comprising said DNA's and a process for their
            preparation, bacterial cultures comprising said recombinant
            plasmids, and method for producing mature thaumatin
  JOURNAL   Patent: EP 0054330-A 4 23-JUN-1982;
            UNILEVER NV; UNILEVER PLC
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          17 GAAG 20
               ||||
Db           9 GAAG 6


RESULT 135
BD238780/c
LOCUS       BD238780                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238780
VERSION     BD238780.1  GI:33048550
KEYWORDS    JP 2002534056-A/198.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 198 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/198
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
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FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           7 TTCT 10
               ||||
Db           8 TTCT 5


RESULT 136
BD238880/c
LOCUS       BD238880                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238880
VERSION     BD238880.1  GI:33048650
KEYWORDS    JP 2002534056-A/298.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 298 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/298
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
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          CC   Preparation and use of superior vaccines
          FH   Key             Location/Qualifiers
          FT   source          1. .10
          FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGG 14
              ||||
Db          6 TGGG 3


RESULT 137
BD240561
LOCUS       BD240561                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240561
VERSION     BD240561.1  GI:33050331
KEYWORDS    JP 2002534056-A/1979.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1979 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1979
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 GAAG 20
              ||||
Db          2 GAAG 5


RESULT 138
I19170
LOCUS       I19170                    10 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 33 from patent US 5502176.
ACCESSION   I19170
VERSION     I19170.1  GI:1599525
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Tenen,D.G., Pahl,H.L. and Burn,T.C.
  TITLE     Myeloid cell specific promoter
  JOURNAL   Patent: US 5502176-A 33 26-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCT 10
              ||||
Db          3 TTCT 6


RESULT 139
AR303345
LOCUS       AR303345                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 70 from patent US 6544736.
ACCESSION   AR303345
VERSION     AR303345.1  GI:31692121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 70 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             20.0%;  Score 4;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCT 10
              ||||
Db          3 TTCT 6


RESULT 140
I34822
LOCUS       I34822                    11 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 15 from patent US 5599673.
ACCESSION   I34822
VERSION     I34822.1  GI:2087790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 11)
  AUTHORS   Keating,M.T., Curran,M.E. and Wang,Q.
  TITLE     Long QT syndrome genes
  JOURNAL   Patent: US 5599673-A 15 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGG 14
              ||||
Db          7 TGGG 10


RESULT 141
AX470593
LOCUS       AX470593                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 170 from Patent WO02053773.
ACCESSION   AX470593
VERSION     AX470593.1  GI:22205718
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 170 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAA 19
              ||||
Db          3 AGAA 6


RESULT 142
AX623377
LOCUS       AX623377                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 418 from Patent WO02053774.
ACCESSION   AX623377
VERSION     AX623377.1  GI:28451318
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 418 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAA 19
              ||||
Db          4 AGAA 7


RESULT 143
AX626059/c
LOCUS       AX626059                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3100 from Patent WO02053774.
ACCESSION   AX626059
VERSION     AX626059.1  GI:28454097
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3100 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAA 19
              ||||
Db         11 AGAA 8


RESULT 144
AX626126
LOCUS       AX626126                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3167 from Patent WO02053774.
ACCESSION   AX626126
VERSION     AX626126.1  GI:28454164
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3167 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGG 14
              ||||
Db          7 TGGG 10


RESULT 145
AX627751
LOCUS       AX627751                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4792 from Patent WO02053774.
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ACCESSION   AX627751
VERSION     AX627751.1  GI:28455789
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4792 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAA 19
              ||||
Db          3 AGAA 6


RESULT 146
AX627837/c
LOCUS       AX627837                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4878 from Patent WO02053774.
ACCESSION   AX627837
VERSION     AX627837.1  GI:28455875
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4878 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAG 17
              ||||
Db          8 GCAG 5


RESULT 147
AX630798
LOCUS       AX630798                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7839 from Patent WO02053774.
ACCESSION   AX630798
VERSION     AX630798.1  GI:28458838
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7839 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGAA 19
              ||||
Db          4 AGAA 7


RESULT 148
AR303500/c
LOCUS       AR303500                 10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 225 from patent US 6544736.
ACCESSION   AR303500
VERSION     AR303500.1  GI:31692276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 225 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           19.0%;  Score 3.8;  DB 1;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
              ||  |||
Db          8 GCTCAAG 2


RESULT 149
AX472203
LOCUS       AX472203                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 194 from Patent WO02053775.
ACCESSION   AX472203
VERSION     AX472203.1  GI:22207240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 194 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           19.0%;  Score 3.8;  DB 1;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
```

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              || |||
Db          4 GCCAAAG 10


RESULT 150
AX471682/c
LOCUS       AX471682                11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1259 from Patent WO02053773.
ACCESSION   AX471682
VERSION     AX471682.1  GI:22206807
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1259 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               | |||
Db           9 ATAAG 5


RESULT 151
AX623509
LOCUS       AX623509                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 550 from Patent WO02053774.
ACCESSION   AX623509
VERSION     AX623509.1  GI:28451450
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 550 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               || ||
Db           2 AGGAG 6


RESULT 152
AX625581
LOCUS       AX625581                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2622 from Patent WO02053774.
ACCESSION   AX625581
VERSION     AX625581.1  GI:28453522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2622 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               | |||
Db           2 AAAAG 6


RESULT 153
AX628191/c
LOCUS       AX628191                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5232 from Patent WO02053774.
ACCESSION   AX628191
VERSION     AX628191.1  GI:28456229
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5232 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          16 AGAAG 20
               | |||
Db           9 ATAAG 5


RESULT 154
AX630930
LOCUS       AX630930                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7971 from Patent WO02053774.
ACCESSION   AX630930
VERSION     AX630930.1  GI:28458972
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7971 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 17.0%; Score 3.4; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         16 AGAAG 20
              || ||
Db          2 AGGAG 6
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Search completed: July 15, 2004, 16:39:01
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 16, 2004, 17:25:19 ; Search time 0.001 Seconds
(without alignments)
21.600 Million cell updates/sec

Title: us-10-024-369-47
Perfect score: 20
Sequence: 1 cccacctttcttgggcagaag 20

Scoring table: IDENTITY
Gapop 10.0 , Gapext 0.5

Searched: 57 seqs, 540 residues

Total number of hits satisfying chosen parameters: 114

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 43 summaries

Database : rnidb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	9	45.0	11	1	US-09-862-847-15	Sequence 15, Appl
	2	9	45.0	12	1	US-09-862-844-6	Sequence 6, Appli
	3	9	45.0	12	1	US-09-862-844-8	Sequence 8, Appli
c	4	8	40.0	9	1	US-09-989-789-2078	Sequence 2078, Ap
c	5	8	40.0	9	1	US-09-989-789-2079	Sequence 2079, Ap
c	6	8	40.0	9	1	US-09-989-789-2262	Sequence 2262, Ap
c	7	8	40.0	9	1	US-09-989-789-2263	Sequence 2263, Ap
c	8	8	40.0	10	1	US-08-410-779B-47	Sequence 47, Appl
c	9	8	40.0	10	1	PCT-US95-04477-47	Sequence 47, Appl
c	10	8	40.0	10	1	US-08-049-283A-31	Sequence 31, Appl
c	11	8	40.0	10	1	US-08-049-283A-33	Sequence 33, Appl
c	12	8	40.0	10	1	US-09-508-753B-70	Sequence 70, Appl
c	13	7	35.0	8	1	US-08-593-345B-19	Sequence 19, Appl
c	14	7	35.0	8	1	US-08-859-954-55	Sequence 55, Appl
c	15	7	35.0	8	1	US-08-859-954-248	Sequence 248, App
c	16	7	35.0	8	1	US-08-859-954-249	Sequence 249, App
c	17	7	35.0	8	1	US-08-859-954-267	Sequence 267, App
c	18	7	35.0	8	1	US-08-859-954-406	Sequence 406, App
c	19	7	35.0	8	1	US-08-859-954-540	Sequence 540, App
c	20	7	35.0	8	1	US-08-855-372B-6	Sequence 6, Appli
c	21	7	35.0	8	1	US-09-498-851-6	Sequence 6, Appli
	22	7	35.0	9	1	US-08-068-945A-36	Sequence 36, Appl
	23	7	35.0	9	1	US-08-442-806-36	Sequence 36, Appl
c	24	7	35.0	9	1	US-09-063-450-10	Sequence 10, Appl
c	25	7	35.0	9	1	US-09-989-789-481	Sequence 481, App
c	26	7	35.0	9	1	US-09-989-789-482	Sequence 482, App
	27	7	35.0	9	1	US-09-989-789-491	Sequence 491, App
	28	7	35.0	9	1	US-09-989-789-492	Sequence 492, App
	29	7	35.0	9	1	US-09-989-789-495	Sequence 495, App
	30	7	35.0	9	1	US-09-989-789-496	Sequence 496, App
	31	7	35.0	9	1	US-09-989-789-497	Sequence 497, App
	32	7	35.0	9	1	US-09-989-789-498	Sequence 498, App
	33	7	35.0	9	1	US-09-989-789-499	Sequence 499, App
	34	7	35.0	9	1	US-09-989-789-577	Sequence 577, App
	35	7	35.0	9	1	US-09-989-789-581	Sequence 581, App
	36	7	35.0	9	1	US-09-989-789-2179	Sequence 2179, Ap
	37	7	35.0	9	1	US-09-989-789-2180	Sequence 2180, Ap
c	38	7	35.0	9	1	US-09-989-789-2233	Sequence 2233, Ap
c	39	7	35.0	9	1	US-09-989-789-2234	Sequence 2234, Ap
c	40	7	35.0	9	1	US-09-989-789-2235	Sequence 2235, Ap
c	41	7	35.0	9	1	US-09-989-789-2264	Sequence 2264, Ap
	42	7	35.0	9	1	US-09-989-789-2355	Sequence 2355, Ap
	43	7	35.0	9	1	US-09-989-789-2358	Sequence 2358, Ap

ALIGNMENTS

RESULT 1
US-09-862-847-15
; Sequence 15, Application US/09862847
; Patent No. 6593111
; GENERAL INFORMATION:
; APPLICANT: Baric, Ralph S.
; APPLICANT: Boyd, Yount
; TITLE OF INVENTION: DIRECTION ASSEMBLY OF LARGE VIRAL GENOMES AND CHROMOSOMES
; FILE REFERENCE: 5470.270
; CURRENT APPLICATION NUMBER: US/09/862,847
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/206,537
; PRIOR FILING DATE: 2000-05-21
; PRIOR APPLICATION NUMBER: US 60/285,320
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer.
US-09-862-847-15

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 CCTTCTTGG 13
              |||||||||
Db          2 CCTTCTTGG 10
```

RESULT 2
US-09-862-844-6
; Sequence 6, Application US/09862844
; Patent No. 6583986
; GENERAL INFORMATION:
; APPLICANT: Cai, Hong
; APPLICANT: Keller, Richard
; APPLICANT: Werner, James
; APPLICANT: Goodwin, Peter
; TITLE OF INVENTION: RAPID HAPLOTYPING BY SINGLE MOLECULE DETECTION
; FILE REFERENCE: S-94,652
; CURRENT APPLICATION NUMBER: US/09/862,844
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: DNA
; ORGANISM: PNA probe MLLCy5P
US-09-862-844-6

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 TTCTTGGGC 15
              |||||||||
Db          2 TTCTTGGGC 10


RESULT 3
US-09-862-844-8
; Sequence 8, Application US/09862844
; Patent No. 6583986
; GENERAL INFORMATION:
;  APPLICANT: Cai, Hong
;  APPLICANT:  Keller, Richard
;  APPLICANT:  Werner, James
;  APPLICANT:  Goodwin, Peter
;  TITLE OF INVENTION: RAPID HAPLOTYPING BY SINGLE MOLECULE DETECTION
;  FILE REFERENCE: S-94,652
;  CURRENT APPLICATION NUMBER: US/09/862,844
;  CURRENT FILING DATE:  2001-05-21
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: LNA probe MLLCy5L
US-09-862-844-8

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGC 15
              |||||||||
Db          2 TTCTTGGGC 10


RESULT 4
US-09-989-789-2078/c
; Sequence 2078, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2078
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2078

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          8 CCCACCTT 1


RESULT 5
US-09-989-789-2079/c
; Sequence 2079, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2079
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2079

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          8 CCCACCTT 1


RESULT 6
US-09-989-789-2262/c
; Sequence 2262, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2262
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2262

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db          9 CACCTTCT 2


RESULT 7
US-09-989-789-2263/c
; Sequence 2263, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2263
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2263

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db          9 CACCTTCT 2


RESULT 8
US-08-410-779B-47/c
; Sequence 47, Application US/08410779B
; Patent No. 5814517
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    TITLE OF INVENTION:  DNA SPACER REGULATORY ELEMENTS
;    TITLE OF INVENTION:  RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  166
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LIGAND PHARMACEUTICALS INCORPORATED
;      STREET:  9393 TOWNE CENTRE DRIVE
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/410,779B
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/228,935
;      FILING DATE:  14-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JURGENSEN, THOMAS E
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0013A.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-410-779B-47

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGG 14
              ||||||||
Db         10 TTCTTGGG 3


RESULT 9
PCT-US95-04477-47/c
; Sequence 47, Application PC/TUS9504477
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
;    TITLE OF INVENTION:  CYTOKINES AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  165
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04477
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/228,935
;      FILING DATE:  14-APR-1994
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
PCT-US95-04477-47

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGG 14
              ||||||||
Db         10 TTCTTGGG 3


RESULT 10
US-08-049-283A-31/c
; Sequence 31, Application US/08049283A
; Patent No. 5502176
;  GENERAL INFORMATION:
;    APPLICANT:  Tenen, Daniel G.
;    APPLICANT:  Pahl, Heike L.
;    APPLICANT:  Burn, Timothy C.
;    TITLE OF INVENTION:  Cell Specific Promoter and Uses Thereof
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.c.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/049,283A
;      FILING DATE:  14-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/020,465
;      FILING DATE:  19-FEB-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/837,776
;      FILING DATE:  13-FEB-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
```

```
;       REGISTRATION NUMBER:  22,592
;       REFERENCE/DOCKET NUMBER:  BIH91-03'A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 861-6240
;       TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-049-283A-31

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
               ||||||||
Db          8 GGCAGAAG 1


RESULT 11
US-08-049-283A-33/c
; Sequence 33, Application US/08049283A
; Patent No. 5502176
;  GENERAL INFORMATION:
;    APPLICANT:  Tenen, Daniel G.
;    APPLICANT:  Pahl, Heike L.
;    APPLICANT:  Burn, Timothy C.
;    TITLE OF INVENTION:  Cell Specific Promoter and Uses Thereof
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.c.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/049,283A
;      FILING DATE:  14-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/020,465
;      FILING DATE:  19-FEB-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/837,776
;      FILING DATE:  13-FEB-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  BIH91-03'A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-049-283A-33

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAA 19
               ||||||||
Db         10 GGGCAGAA 3


RESULT 12
US-09-508-753B-70/c
; Sequence 70, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 70
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-70

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAA 19
               ||||||||
Db         10 GGGCAGAA 3


RESULT 13
US-08-593-345B-19/c
; Sequence 19, Application US/08593345B
; Patent No. 5851772
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Lysov, Yuriy P
;    APPLICANT:  Shick, Valentine V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  A Microchip Method for the Enrichment of
;    TITLE OF INVENTION:  Specific DNA Sequences.
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/593,345B
;      FILING DATE:  29-JAN-96
;    PRIOR APPLICATION DATA:  No. 5851772e
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Cherskov, Michael J.
;       REGISTRATION NUMBER:  33,664
;       REFERENCE/DOCKET NUMBER:  ANL-IN-95-029+30
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 621-1330
;       TELEFAX:  (312) 621-0088
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  No. 5851772 Applicable
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  Genomic DNA
;     FEATURE:
;       NAME/KEY:  No. 5851772e
;       LOCATION:  1-8
;       IDENTIFICATION METHOD:  Similarity with known sequences.
;       OTHER INFORMATION:  Complementarity with primer of
;       OTHER INFORMATION:  exons to a-thalassemia gene.
US-08-593-345B-19

  Query Match           35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TCTTGGG 14
              |||||||
Db          7 TCTTGGG 1


RESULT 14
US-08-859-954-55/c
; Sequence 55, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-55

  Query Match           35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 TTGGGCA 16
               |||||||
Db           8 TTGGGCA 2


RESULT 15
US-08-859-954-248/c
; Sequence 248, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  248:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-248

  Query Match           35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTC 9
              |||||||
Db          7 CACCTTC 1
```

```
RESULT 16
US-08-859-954-249/c
; Sequence 249, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  249:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-249

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTC 9
              |||||||
Db          7 CACCTTC 1


RESULT 17
US-08-859-954-267/c
; Sequence 267, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  267:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-267

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTT 11
              |||||||
Db          8 CCTTCTT 2


RESULT 18
US-08-859-954-406/c
; Sequence 406, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  406:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-406

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 TTGGGCA 16
              |||||||
Db          8 TTGGGCA 2


RESULT 19
US-08-859-954-540/c
; Sequence 540, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  540:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-540

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTT 8
              |||||||
Db          7 CCACCTT 1


RESULT 20
US-08-855-372B-6/c
; Sequence 6, Application US/08855372B
; Patent No. 6090549
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous Stacking Hybridization as a Diagn
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/855,372B
;      FILING DATE:  13-MAY-97
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6090549 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-08-855-372B-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGCAG 17
              |||||||
Db          7 TGGGCAG 1


RESULT 21
US-09-498-851-6/c
; Sequence 6, Application US/09498851
; Patent No. 6440671
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous
;    TITLE OF INVENTION:  Stacking Hybridization as a Diagnostic Tool.
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/498,851
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/855,372
;      FILING DATE:  13-MAY-97
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6440671 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-09-498-851-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGGCAG 17
               |||||||
Db           7 TGGGCAG 1


RESULT 22
US-08-068-945A-36
; Sequence 36, Application US/08068945A
; Patent No. 5616483
;  GENERAL INFORMATION:
;    APPLICANT:  Bjursell, Gunnar
;    APPLICANT:  Carlsson, Peter
;    APPLICANT:  Enerback, Sven
;    APPLICANT:  Hansson, Lennart
;    APPLICANT:  Lidberg, Ulf
;    APPLICANT:  Nilsson, Jeanette
;    APPLICANT:  Tornell, Jan
;    TITLE OF INVENTION:  New DNA Sequences
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White & Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,945A
;      FILING DATE:  27-MAY-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9201809-2
;      FILING DATE:  11-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9201826-6
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9202088-2
;      FILING DATE:  03-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9300902-5
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J.
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-052
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8783
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-068-945A-36

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGG 13
               |||||||
Db          2 TTCTTGG 8


RESULT 23
US-08-442-806-36
; Sequence 36, Application US/08442806
; Patent No. 5716817
;  GENERAL INFORMATION:
;    APPLICANT:  Bjursell, Gunnar
;    APPLICANT:  Carlsson, Peter
;    APPLICANT:  Enerback, Sven
;    APPLICANT:  Hansson, Lennart
;    APPLICANT:  Lidberg, Ulf
;    APPLICANT:  Nilsson, Jeanette
;    APPLICANT:  Tornell, Jan
;    TITLE OF INVENTION:  Genomic DNA Sequences
;    TITLE OF INVENTION:  Encoding Human BSSL/CEL
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White & Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/442,806
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/068,945
;       FILING DATE:  27-MAY-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  SE 9201809-2
;       FILING DATE:  11-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  SE 9201826-6
;       FILING DATE:  12-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  SE 9202088-2
;       FILING DATE:  03-JUL-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  SE 9300902-5
;       FILING DATE:  19-MAR-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sterner, Richard J.
;       REGISTRATION NUMBER:  35,372
;       REFERENCE/DOCKET NUMBER:  1103326-052
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)819-8783
;       TELEFAX:  (212)354-8113
;   INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9,base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-442-806-36

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGG 13
              |||||||
Db          2 TTCTTGG 8


RESULT 24
US-09-063-450-10/c
; Sequence 10, Application US/09063450
; Patent No. 6109776
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: Method and System for Computationally Identifying
;  TITLE OF INVENTION: Clusters Within a Set of Sequences
;  FILE REFERENCE: 77001.002
;  CURRENT APPLICATION NUMBER: US/09/063,450
;  CURRENT FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:example
;   OTHER INFORMATION: sequence illustrating a computational methodology
US-09-063-450-10

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTC 9
              |||||||
Db          9 CACCTTC 3


RESULT 25
US-09-989-789-481/c
; Sequence 481, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 481
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-481

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTT 11
              |||||||
Db          8 CCTTCTT 2


RESULT 26
US-09-989-789-482/c
; Sequence 482, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 482
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-482

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTT 11
              |||||||
Db          8 CCTTCTT 2


RESULT 27
US-09-989-789-491
; Sequence 491, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
```

```
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 491
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-491

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
               |||||||
Db          1 GCAGAAG 7


RESULT 28
US-09-989-789-492
; Sequence 492, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 492
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-492

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
               |||||||
Db          1 GCAGAAG 7


RESULT 29
US-09-989-789-495
; Sequence 495, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 495
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-495

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
               |||||||
Db          1 GCAGAAG 7


RESULT 30
US-09-989-789-496
; Sequence 496, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 496
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-496

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
               |||||||
Db          1 GCAGAAG 7


RESULT 31
US-09-989-789-497
; Sequence 497, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 497
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-497

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
```

```
              |||||||
Db          1 GCAGAAG 7


RESULT 32
US-09-989-789-498
; Sequence 498, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 498
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-498

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
              |||||||
Db          1 GCAGAAG 7


RESULT 33
US-09-989-789-499
; Sequence 499, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 499
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-499

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
              |||||||
Db          1 GCAGAAG 7


RESULT 34
US-09-989-789-577
; Sequence 577, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 577
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-577

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
              |||||||
Db          1 GCAGAAG 7


RESULT 35
US-09-989-789-581
; Sequence 581, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 581
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-581

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GCAGAAG 20
              |||||||
Db          1 GCAGAAG 7


RESULT 36
US-09-989-789-2179
; Sequence 2179, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2179
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2179

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAA 19
              |||||||
Db          3 GGCAGAA 9


RESULT 37
US-09-989-789-2180
; Sequence 2180, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2180
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2180

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAA 19
              |||||||
Db          3 GGCAGAA 9


RESULT 38
US-09-989-789-2233/c
; Sequence 2233, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2233
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2233

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTC 9
              |||||||
Db          9 CACCTTC 3


RESULT 39
US-09-989-789-2234/c
; Sequence 2234, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2234
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2234

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTC 9
              |||||||
Db          9 CACCTTC 3


RESULT 40
US-09-989-789-2235/c
; Sequence 2235, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2235
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2235

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTC 9
              |||||||
Db          9 CACCTTC 3


RESULT 41
US-09-989-789-2264/c
; Sequence 2264, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
```

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;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2264
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2264

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTC 9
              |||||||
Db          7 CACCTTC 1


RESULT 42
US-09-989-789-2355
; Sequence 2355, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2355
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2355

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGCAG 17
              |||||||
Db          1 TGGGCAG 7


RESULT 43
US-09-989-789-2358
; Sequence 2358, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2358
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2358

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGCAG 17
              |||||||
Db          1 TGGGCAG 7


Search completed: July 16, 2004, 17:25:19
Job time : 0.001 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 15, 2004, 18:05:04 ; Search time 0.001 Seconds
(without alignments)
72.760 Million cell updates/sec

Title: us-10-024-369-47
Perfect score: 20
Sequence: 1 cccaccttcttgggcagaag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 169 seqs, 1819 residues

Total number of hits satisfying chosen parameters: 338

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2000 summaries

Database : rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	AAL62417	Human ABC transpor
	2	12	60.0	15	1	ABA96458	Human IL-2 probe S
c	3	11.8	59.0	15	1	AAF45929	IGFBP2 oligonucleo
c	4	11.4	57.0	15	1	AAF45927	IGFBP2 oligonucleo
c	5	11.4	57.0	15	1	AAF45928	IGFBP2 oligonucleo
c	6	11	55.0	13	1	ABC34320	Oligonucleotide SE
	7	11	55.0	13	1	ABC34321	Oligonucleotide SE
c	8	11	55.0	13	1	ABC45614	Oligonucleotide SE
	9	11	55.0	13	1	ABC45615	Oligonucleotide SE
c	10	10	50.0	10	1	AAZ81481	Metastatic breast
	11	10	50.0	11	1	ABV70040	Human skin EST 782
	12	10	50.0	11	1	ABV62619	Human skin EST 405
	13	10	50.0	12	1	ABH76170	Oligonucleotide pr
	14	10	50.0	12	1	ABI71877	Oligonucleotide pr
c	15	10	50.0	13	1	AAA54180	5' exon-intron jun
	16	9.8	49.0	13	1	ABC48640	Oligonucleotide SE
c	17	9.8	49.0	13	1	ABC48641	Oligonucleotide SE
c	18	9.8	49.0	13	1	ABF26997	Oligonucleotide SE
	19	9.8	49.0	13	1	ABF26996	Oligonucleotide SE
c	20	9.4	47.0	11	1	ABK99486	Human CYP3A5 gene
	21	9.4	47.0	12	1	ABI13302	Oligonucleotide pr
c	22	9.4	47.0	12	1	ABI47015	Oligonucleotide pr
c	23	9.4	47.0	12	1	ABI45565	Oligonucleotide pr
c	24	9.4	47.0	12	1	ABI69022	Oligonucleotide pr
	25	9.4	47.0	12	1	ABH91427	Oligonucleotide pr
c	26	9.4	47.0	12	1	ABI61189	Oligonucleotide pr
	27	9.4	47.0	12	1	ABH98731	Oligonucleotide pr
c	28	9.4	47.0	12	1	ABH85586	Oligonucleotide pr
c	29	9	45.0	10	1	AAZ77982	Human dendritic ce
c	30	9	45.0	10	1	AAZ78502	Human dendritic ce
c	31	9	45.0	10	1	AAZ78803	Human dendritic ce
c	32	9	45.0	10	1	AAZ82426	Metastatic breast
c	33	9	45.0	10	1	AAF42275	Yeast NORF gene SA
	34	9	45.0	10	1	ABT14287	Nucleic acid PCR a
	35	9	45.0	11	1	AAA87795	Promoter P15B3 tra
	36	9	45.0	11	1	AAS07926	Human transcriptio
	37	9	45.0	11	1	ABV64418	Human skin EST 220
	38	9	45.0	11	1	ABV71839	Human skin EST 962
	39	9	45.0	11	1	AAK99270	P15B4 promoter tra
	40	9	45.0	11	1	AAS21210	Transmissible gast
c	41	9	45.0	12	1	ABI19388	Oligonucleotide pr
c	42	9	45.0	12	1	ABI08577	Oligonucleotide pr
c	43	9	45.0	12	1	ABI25588	Oligonucleotide pr
c	44	9	45.0	12	1	ABI13144	Oligonucleotide pr
	45	9	45.0	12	1	ABI48769	Oligonucleotide pr
	46	9	45.0	12	1	ABH88612	Oligonucleotide pr
c	47	9	45.0	12	1	ABI67143	Oligonucleotide pr
	48	9	45.0	12	1	ABH94365	Oligonucleotide pr
	49	9	45.0	12	1	ABH96358	Oligonucleotide pr
c	50	9	45.0	12	1	ABH74429	Oligonucleotide pr
c	51	9	45.0	12	1	ABH70993	Oligonucleotide pr
	52	9	45.0	12	1	ABH88613	Oligonucleotide pr
	53	9	45.0	12	1	ABI52693	Oligonucleotide pr
c	54	9	45.0	12	1	ABI40468	Oligonucleotide pr
c	55	9	45.0	12	1	ABI10163	Oligonucleotide pr
	56	9	45.0	12	1	ABH94363	Oligonucleotide pr
c	57	9	45.0	12	1	ABI73341	Oligonucleotide pr
	58	9	45.0	12	1	AAD25619	MLLCy5L LNA probe
	59	9	45.0	12	1	AAD25617	MLLCy5P PNA probe
c	60	8.4	42.0	10	1	AAT14161	Cytokine responsiv
c	61	8.4	42.0	10	1	AAV56888	Regulatory element
c	62	8.4	42.0	10	1	AAZ79653	Human dendritic ce
	63	8.4	42.0	10	1	AAZ77834	Human dendritic ce
	64	8.4	42.0	10	1	AAZ78009	Human dendritic ce
c	65	8.4	42.0	10	1	AAZ84938	Metastatic breast
	66	8.4	42.0	10	1	AAZ85708	Metastatic breast
	67	8.4	42.0	10	1	AAZ81181	Metastatic breast
	68	8.4	42.0	10	1	AAZ80869	Metastatic breast
	69	8.4	42.0	10	1	AAZ79893	Human dendritic ce
c	70	8.4	42.0	10	1	AAA73656	Probe #25 for sequ
c	71	8.4	42.0	10	1	AAH63873	Human ubiquitously
	72	8.4	42.0	10	1	AAF43792	Yeast NORF gene SA
c	73	8.4	42.0	10	1	AAF34723	Yeast NORF gene SA
c	74	8.4	42.0	10	1	AAF38664	Yeast NORF gene SA
c	75	8.4	42.0	10	1	AAF37520	Yeast NORF gene SA
c	76	8.4	42.0	10	1	AAF37547	Yeast NORF gene SA
	77	8.4	42.0	10	1	AAF40919	Yeast NORF gene SA
c	78	8.4	42.0	10	1	AAF38830	Yeast NORF gene SA
c	79	8.4	42.0	10	1	AAF41899	Yeast NORF gene SA
c	80	8.4	42.0	10	1	AAF40814	Yeast NORF gene SA
c	81	8.4	42.0	10	1	ABL88354	Human CHRNE gene p
	82	8.4	42.0	10	1	ABK37010	Human ALAS2 gene a
c	83	8.4	42.0	10	1	ABL39516	Human ETFB primer-
	84	8.4	42.0	10	1	ABL52253	Human PHKG2 prefer
c	85	8.4	42.0	10	1	ABL52252	Human PHKG2 prefer
	86	8.4	42.0	10	1	ABV78454	Human transcriptio
c	87	8.4	42.0	10	1	ABV84246	Human mitochondria
c	88	8.4	42.0	10	1	ABK23703	Transcript tag DNA
	89	8.4	42.0	10	1	ABN84506	Rat smooth muscle
	90	8.4	42.0	10	1	ACA60848	Rat smooth muscle
	91	8.4	42.0	10	1	ABQ72900	Human GRM8 gene po
	92	8.4	42.0	10	1	ABK96537	Human PLAU gene, p
c	93	8.4	42.0	10	1	ACF04526	Stuffer sequence u
c	94	8.4	42.0	11	1	AAA16595	Human MN gene 5' d
c	95	8.4	42.0	11	1	AAA52514	Human MN gene intr
	96	8.4	42.0	11	1	ABQ87504	Human skin stress/
	97	8.4	42.0	11	1	ABQ87500	Human skin stress/
c	98	8.4	42.0	11	1	ABQ86415	Human skin stress/
c	99	8.4	42.0	11	1	ABV66344	Human skin EST 413
c	100	8.4	42.0	11	1	ABV62764	Human skin EST 550
c	101	8.4	42.0	11	1	ABV70185	Human skin EST 797
	102	8.4	42.0	11	1	ABV62651	Human skin EST 437
c	103	8.4	42.0	11	1	ABV67006	Human skin EST 479
	104	8.4	42.0	11	1	ABV67047	Human skin EST 483
c	105	8.4	42.0	11	1	ABV64836	Human skin EST 262
	106	8.4	42.0	11	1	ABV67092	Human skin EST 487

	107	8.4	42.0	11	1	ABV67518	Human skin EST 530
	108	8.4	42.0	11	1	ABV72108	Human skin EST 989
c	109	8.4	42.0	11	1	ABV62632	Human skin EST 418
c	110	8.4	42.0	11	1	ABV65381	Human skin EST 316
	111	8.4	42.0	11	1	ABV67446	Human skin EST 523
	112	8.4	42.0	11	1	ABV66204	Human skin EST 399
	113	8.4	42.0	11	1	ABV65314	Human skin EST 310
	114	8.4	42.0	11	1	ABV70072	Human skin EST 785
c	115	8.4	42.0	11	1	ABV69202	Human skin EST 698
c	116	8.4	42.0	11	1	ABV70053	Human skin EST 783
c	117	8	40.0	8	1	AAT09397	5'-primer used for
	118	8	40.0	8	1	AAT09546	3'-primer used for
c	119	8	40.0	8	1	AAT09415	5'-primer used for
	120	8	40.0	8	1	AAT09568	3'-primer used for
c	121	8	40.0	9	1	ABQ71965	Zinc finger protei
c	122	8	40.0	9	1	ABQ71964	Zinc finger protei
c	123	8	40.0	9	1	ABQ71781	Zinc finger protei
c	124	8	40.0	9	1	ABQ71780	Zinc finger protei
	125	8	40.0	9	1	ACD06034	Human VEGF-targete
	126	8	40.0	9	1	ACD19256	Human VEGF-targete
c	127	8	40.0	9	1	ADA64108	Zinc finger target
c	128	8	40.0	9	1	ADA64291	Zinc finger target
c	129	8	40.0	9	1	ADA64292	Zinc finger target
c	130	8	40.0	9	1	ADA64107	Zinc finger target
c	131	8	40.0	10	1	AAZ79378	Human dendritic ce
	132	8	40.0	10	1	AAZ77868	Human dendritic ce
c	133	8	40.0	10	1	AAZ78273	Human dendritic ce
	134	8	40.0	10	1	AAZ78942	Human dendritic ce
	135	8	40.0	10	1	AAZ77770	Human dendritic ce
	136	8	40.0	10	1	AAZ77870	Human dendritic ce
	137	8	40.0	10	1	AAZ79364	Human dendritic ce
c	138	8	40.0	10	1	AAZ79551	Human dendritic ce
	139	8	40.0	10	1	AAZ83134	Metastatic breast
	140	8	40.0	10	1	AAZ81919	Metastatic breast
c	141	8	40.0	10	1	AAZ84193	Metastatic breast
c	142	8	40.0	10	1	AAZ82122	Metastatic breast
	143	8	40.0	10	1	AAZ83647	Metastatic breast
	144	8	40.0	10	1	AAZ83418	Metastatic breast
c	145	8	40.0	10	1	AAZ82784	Metastatic breast
	146	8	40.0	10	1	AAZ85883	Metastatic breast
c	147	8	40.0	10	1	AAZ86535	Metastatic breast
c	148	8	40.0	10	1	AAZ81064	Metastatic breast
c	149	8	40.0	10	1	AAZ83296	Metastatic breast
c	150	8	40.0	10	1	AAZ84897	Metastatic breast
	151	8	40.0	10	1	AAZ81128	Metastatic breast
c	152	8	40.0	10	1	AAZ83682	Metastatic breast
c	153	8	40.0	10	1	AAZ83851	Metastatic breast
	154	8	40.0	10	1	AAZ79914	Human dendritic ce
c	155	8	40.0	10	1	AAH64317	Human ubiquitously
	156	8	40.0	10	1	AAH63292	Human colon epithe
c	157	8	40.0	10	1	AAF69638	Human IL4Ralpha ge
c	158	8	40.0	10	1	AAF35751	Yeast NORF gene SA
	159	8	40.0	10	1	AAF39472	Yeast NORF gene SA
	160	8	40.0	10	1	AAF39102	Yeast NORF gene SA
	161	8	40.0	10	1	AAF41579	Yeast NORF gene SA
c	162	8	40.0	10	1	AAF43940	Yeast NORF gene SA
c	163	8	40.0	10	1	AAF34735	Yeast NORF gene SA
c	164	8	40.0	10	1	AAF34229	Yeast NORF gene SA
c	165	8	40.0	10	1	AAF37328	Yeast NORF gene SA
c	166	8	40.0	10	1	ABK24258	Retinaldehyde-bind
c	167	8	40.0	10	1	ABK23697	Transcript tag DNA
	168	8	40.0	10	1	AAS16818	Human apolipoprote
	169	8	40.0	10	1	ADC09948	Optical nucleic ac
c	170	7	35.0	20	1	AAL62417	Human ABC transpor
c	171	6.4	32.0	12	1	ABH88612	Oligonucleotide pr
c	172	6.4	32.0	12	1	ABH88613	Oligonucleotide pr
	173	6	30.0	10	1	AAZ79378	Human dendritic ce
c	174	6	30.0	10	1	AAZ77868	Human dendritic ce
	175	6	30.0	10	1	AAZ82122	Metastatic breast
c	176	6	30.0	10	1	AAZ83647	Metastatic breast
	177	6	30.0	10	1	AAZ84897	Metastatic breast
	178	6	30.0	10	1	AAH64317	Human ubiquitously
c	179	6	30.0	11	1	ABV64418	Human skin EST 220
c	180	6	30.0	11	1	ABV71839	Human skin EST 962
c	181	6	30.0	11	1	ABQ87500	Human skin stress/
c	182	6	30.0	11	1	ABV67047	Human skin EST 483
	183	5.4	27.0	10	1	AAZ84938	Metastatic breast
	184	5.4	27.0	10	1	AAH63873	Human ubiquitously
	185	5.4	27.0	10	1	AAF37520	Yeast NORF gene SA
	186	5.4	27.0	10	1	ABV84246	Human mitochondria
	187	5.4	27.0	10	1	ABK23703	Transcript tag DNA
c	188	5.4	27.0	10	1	AAZ78942	Human dendritic ce
	189	5.4	27.0	10	1	AAF34229	Yeast NORF gene SA
	190	5.4	27.0	11	1	ABV69202	Human skin EST 698
	191	5.4	27.0	12	1	ABI08577	Oligonucleotide pr
	192	5.4	27.0	12	1	ABI13144	Oligonucleotide pr
c	193	5.4	27.0	12	1	ABH96358	Oligonucleotide pr
	194	5.4	27.0	13	1	ABC34320	Oligonucleotide SE
c	195	5.4	27.0	13	1	ABC34321	Oligonucleotide SE
	196	5.4	27.0	13	1	ABC45614	Oligonucleotide SE
c	197	5.4	27.0	13	1	ABC45615	Oligonucleotide SE
	198	5.2	26.0	11	1	ABV66344	Human skin EST 413
c	199	5.2	26.0	11	1	ABV72108	Human skin EST 989
c	200	5.2	26.0	11	1	ABV66204	Human skin EST 399
	201	5	25.0	8	1	AAT09397	5'-primer used for
c	202	5	25.0	8	1	AAT09546	3'-primer used for
	203	5	25.0	8	1	AAT09415	5'-primer used for
c	204	5	25.0	8	1	AAT09568	3'-primer used for
	205	5	25.0	9	1	ABQ71965	Zinc finger protei
	206	5	25.0	9	1	ABQ71964	Zinc finger protei
	207	5	25.0	9	1	ABQ71781	Zinc finger protei
	208	5	25.0	9	1	ABQ71780	Zinc finger protei
	209	5	25.0	9	1	ADA64108	Zinc finger target
	210	5	25.0	9	1	ADA64291	Zinc finger target
	211	5	25.0	9	1	ADA64292	Zinc finger target
	212	5	25.0	9	1	ADA64107	Zinc finger target
	213	5	25.0	10	1	AAZ81481	Metastatic breast
	214	5	25.0	10	1	AAZ78803	Human dendritic ce
	215	5	25.0	10	1	AAZ82426	Metastatic breast
	216	5	25.0	10	1	AAF42275	Yeast NORF gene SA
c	217	5	25.0	10	1	AAZ80869	Metastatic breast
	218	5	25.0	10	1	AAF34723	Yeast NORF gene SA
	219	5	25.0	10	1	AAF41899	Yeast NORF gene SA
	220	5	25.0	10	1	AAF40814	Yeast NORF gene SA
c	221	5	25.0	10	1	ABQ72900	Human GRM8 gene po
	222	5	25.0	10	1	AAZ78273	Human dendritic ce
c	223	5	25.0	10	1	AAZ79364	Human dendritic ce
c	224	5	25.0	10	1	AAZ83134	Metastatic breast
	225	5	25.0	10	1	AAZ83296	Metastatic breast
c	226	5	25.0	10	1	AAH63292	Human colon epithe
	227	5	25.0	10	1	AAF35751	Yeast NORF gene SA
c	228	5	25.0	10	1	AAF39472	Yeast NORF gene SA
c	229	5	25.0	10	1	AAF41579	Yeast NORF gene SA
	230	5	25.0	10	1	AAF34735	Yeast NORF gene SA
	231	5	25.0	10	1	AAF37328	Yeast NORF gene SA
	232	5	25.0	10	1	ABK23697	Transcript tag DNA
c	233	5	25.0	11	1	ABV70040	Human skin EST 782
c	234	5	25.0	11	1	ABV62619	Human skin EST 405
c	235	5	25.0	11	1	AAS21210	Transmissible gast
	236	5	25.0	11	1	AAA16595	Human MN gene 5' d
	237	5	25.0	11	1	AAA52514	Human MN gene intr
c	238	5	25.0	11	1	ABV62651	Human skin EST 437
c	239	5	25.0	11	1	ABV70072	Human skin EST 785
c	240	5	25.0	12	1	ABH76170	Oligonucleotide pr
c	241	5	25.0	12	1	ABI71877	Oligonucleotide pr
c	242	5	25.0	12	1	ABH91427	Oligonucleotide pr
	243	5	25.0	12	1	ABI61189	Oligonucleotide pr
	244	5	25.0	12	1	ABH85586	Oligonucleotide pr
	245	5	25.0	12	1	ABI19388	Oligonucleotide pr
	246	5	25.0	12	1	ABI25588	Oligonucleotide pr
	247	5	25.0	12	1	ABI67143	Oligonucleotide pr
c	248	5	25.0	12	1	ABH94365	Oligonucleotide pr
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	250	5	25.0	12	1	ABI40468	Oligonucleotide pr
	251	5	25.0	12	1	ABI10163	Oligonucleotide pr
c	252	5	25.0	12	1	ABH94363	Oligonucleotide pr

	253	5	25.0	12	1	ABI73341	Oligonucleotide pr
	254	5	25.0	13	1	AAA54180	5' exon-intron jun
c	255	5	25.0	13	1	ABC48640	Oligonucleotide SE
	256	5	25.0	13	1	ABC48641	Oligonucleotide SE
c	257	5	25.0	15	1	ABA96458	Human IL-2 probe S
	258	5	25.0	15	1	AAF45929	IGFBP2 oligonucleo
	259	5	25.0	15	1	AAF45927	IGFBP2 oligonucleo
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	261	4.4	22.0	10	1	ABL88354	Human CHRNE gene p
c	262	4.4	22.0	10	1	ABV78454	Human transcriptio
	263	4.4	22.0	10	1	AAF69638	Human IL4Ralpha ge
c	264	4.4	22.0	11	1	ABV67518	Human skin EST 530
c	265	4.4	22.0	12	1	ABI48769	Oligonucleotide pr
	266	4.4	22.0	13	1	ABF26997	Oligonucleotide SE
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	269	4.2	21.0	10	1	ABK24258	Retinaldehyde-bind
c	270	4.2	21.0	12	1	AAD25619	MLLCy5L LNA probe
c	271	4.2	21.0	12	1	AAD25617	MLLCy5P PNA probe
c	272	4	20.0	9	1	ACD06034	Human VEGF-targete
c	273	4	20.0	9	1	ACD19256	Human VEGF-targete
	274	4	20.0	10	1	AAZ77982	Human dendritic ce
	275	4	20.0	10	1	AAZ78502	Human dendritic ce
c	276	4	20.0	10	1	ABT14287	Nucleic acid PCR a
	277	4	20.0	10	1	AAT14161	Cytokine responsiv
	278	4	20.0	10	1	AAV56888	Regulatory element
	279	4	20.0	10	1	AAZ79653	Human dendritic ce
c	280	4	20.0	10	1	AAZ77834	Human dendritic ce
c	281	4	20.0	10	1	AAZ78009	Human dendritic ce
c	282	4	20.0	10	1	AAZ85708	Metastatic breast
c	283	4	20.0	10	1	AAZ79893	Human dendritic ce
	284	4	20.0	10	1	AAA73656	Probe #25 for sequ
c	285	4	20.0	10	1	AAF43792	Yeast NORF gene SA
	286	4	20.0	10	1	AAF37547	Yeast NORF gene SA
c	287	4	20.0	10	1	AAF40919	Yeast NORF gene SA
	288	4	20.0	10	1	AAF38830	Yeast NORF gene SA
c	289	4	20.0	10	1	ABK37010	Human ALAS2 gene a
	290	4	20.0	10	1	ABL39516	Human ETFB primer-
c	291	4	20.0	10	1	ABL52253	Human PHKG2 prefer
	292	4	20.0	10	1	ABL52252	Human PHKG2 prefer
c	293	4	20.0	10	1	ABN84506	Rat smooth muscle
c	294	4	20.0	10	1	ACA60848	Rat smooth muscle
c	295	4	20.0	10	1	ABK96537	Human PLAU gene, p
	296	4	20.0	10	1	ACF04526	Stuffer sequence u
c	297	4	20.0	10	1	AAZ77770	Human dendritic ce
c	298	4	20.0	10	1	AAZ77870	Human dendritic ce
	299	4	20.0	10	1	AAZ79551	Human dendritic ce
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	301	4	20.0	10	1	AAZ84193	Metastatic breast
c	302	4	20.0	10	1	AAZ83418	Metastatic breast
	303	4	20.0	10	1	AAZ82784	Metastatic breast
c	304	4	20.0	10	1	AAZ85883	Metastatic breast
	305	4	20.0	10	1	AAZ86535	Metastatic breast
	306	4	20.0	10	1	AAZ81064	Metastatic breast
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	308	4	20.0	10	1	AAZ83682	Metastatic breast
	309	4	20.0	10	1	AAZ83851	Metastatic breast
c	310	4	20.0	10	1	AAZ79914	Human dendritic ce
c	311	4	20.0	10	1	AAF39102	Yeast NORF gene SA
	312	4	20.0	10	1	AAF43940	Yeast NORF gene SA
c	313	4	20.0	10	1	AAS16818	Human apolipoprote
c	314	4	20.0	10	1	ADC09948	Optical nucleic ac
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c	317	4	20.0	11	1	AAK99270	P15B4 promoter tra
	318	4	20.0	11	1	ABQ86415	Human skin stress/
	319	4	20.0	11	1	ABV67006	Human skin EST 479
c	320	4	20.0	11	1	ABV67092	Human skin EST 487
	321	4	20.0	11	1	ABV62632	Human skin EST 418
	322	4	20.0	11	1	ABV65381	Human skin EST 316
c	323	4	20.0	11	1	ABV65314	Human skin EST 310
	324	4	20.0	11	1	ABV70053	Human skin EST 783
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	326	4	20.0	12	1	ABI47015	Oligonucleotide pr
	327	4	20.0	12	1	ABI45565	Oligonucleotide pr
	328	4	20.0	12	1	ABI69022	Oligonucleotide pr
c	329	4	20.0	12	1	ABH98731	Oligonucleotide pr
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	331	4	20.0	12	1	ABH70993	Oligonucleotide pr
	332	3.8	19.0	11	1	ABK99486	Human CYP3A5 gene
	333	3.4	17.0	10	1	AAF38664	Yeast NORF gene SA
c	334	3.4	17.0	11	1	ABQ87504	Human skin stress/
	335	3.4	17.0	11	1	ABV62764	Human skin EST 550
	336	3.4	17.0	11	1	ABV70185	Human skin EST 797
	337	3.4	17.0	11	1	ABV64836	Human skin EST 262
c	338	3.4	17.0	11	1	ABV67446	Human skin EST 523

ALIGNMENTS

RESULT 1
AAL62417
ID AAL62417 standard; DNA; 20 BP.
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AC AAL62417;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human ABC transporter MHC I antisense oligonucleotide, ISIS 206598.
XX
KW ABC transporter; ABCT; major histocompatibility complex; MHC; cytostatic;
KW hyperproliferative; autoimmune disorder; antisense gene therapy;
KW inflammation; tumour formation; immunosuppressive; antimicrobial; human;
KW phosphorothioate backbone; antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
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FT methylcytidines"
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XX
PN WO2003051309-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040101.
XX
PR 17-DEC-2001; 2001US-00024369.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Borchers AH, Ward DT, Freier SM;
XX
DR WPI; 2003-577305/54.
XX
PT New antisense compound that hybridizes and inhibits the nucleic acid
PT encoding ABC transporter major histocompatibility complex 1, for treating
PT diseases or conditions such as a hyperproliferative or autoimmune
PT disorder.
XX
PS Claim 3; Page 81; 112pp; English.
XX
CC The invention relates to a compound targetted to a nucleic acid molecule

```
CC   encoding ABC transporter (ABCT) major histocompatibility complex (MHC) 1
CC   where the compound specifically hybridises with the nucleic acid molecule
CC   and inhibits expression of ATM or specifically hybridises with at least a
CC   portion of an active site on the nucleic acid molecule. The invention is
CC   useful for inhibiting the expression of ATM in cells or tissues. The
CC   invention is useful for treating an animal with hyperproliferative or
CC   autoimmune disorder. The invention is useful for diagnostics,
CC   therapeutics, prophylaxis, as research reagents and kits, for
CC   distinguishing functions of various members of a biological pathway and
CC   in antisense gene therapy. The invention is also useful prophylactically
CC   e.g., to prevent or delay infection, inflammation or tumour formation.
CC   The present sequence is an antisense oligo targetted to human ABC
CC   transporter MHC I DNA. This sequence is used to illustrate the method of
CC   the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTTGGGCAGAAG 20
              ||||||||||||||||||||
Db          1 CCCACCTTCTTGGGCAGAAG 20


RESULT 2
ABA96458
ID   ABA96458 standard; DNA; 15 BP.
XX
AC   ABA96458;
XX
DT   03-APR-2002  (first entry)
XX
DE   Human IL-2 probe SEQ ID NO 2.
XX
KW   Human; IL-2; IL-4; probe; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001286285-A.
XX
PD   16-OCT-2001.
XX
PF   28-APR-2000; 2000JP-00130793.
XX
PR   04-FEB-2000; 2000JP-00028117.
XX
PA   (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
XX
DR   WPI; 2002-134187/18.
XX
PT   Selective separation of live cells expressing a specific gene.
XX
PS   Example; Page 9; 65pp; Japanese.
XX
CC   The invention relates to selectively separating live cells expressing a
CC   specific gene and involves introducing a labelling agent which can label
CC   a specific mRNA in the cells of a live cell group expressing the mRNA.
CC   The method is used for selectively separating live cells expressing a
CC   specific gene. The present sequence is that of a human IL-2 probe
XX
SQ   Sequence 15 BP; 1 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match            60.0%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 9.5;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTGGGCA 16
              ||||||||||||
Db          3 CCTTCTTGGGCA 14


RESULT 3
AAF45929/c
ID   AAF45929 standard; DNA; 15 BP.
XX
AC   AAF45929;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #768.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 5 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match            59.0%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity  86.7%;  Pred. No. 11;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTTGGGC 15
              | || ||||||||||
Db         15 CGCAGCTTCTTGGGC 1


RESULT 4
AAF45927/c
ID   AAF45927 standard; DNA; 15 BP.
XX
```

```
AC   AAF45927;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #766.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 5 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 14;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTGGGC 15
              || ||||||||||
Db         15 CAGCTTCTTGGGC 3


RESULT 5
AAF45928/c
ID   AAF45928 standard; DNA; 15 BP.
XX
AC   AAF45928;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #767.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 5 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 14;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTGGGC 15
              || ||||||||||
Db         14 CAGCTTCTTGGGC 2


RESULT 6
ABC34320/c
ID   ABC34320 standard; DNA; 13 BP.
XX
AC   ABC34320;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 34337 for detecting SNP TSC0010965.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

```
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 34337; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||||||||||
Db         13 CCCACCTTCTT 3


RESULT 7
ABC34321
ID   ABC34321 standard; DNA; 13 BP.
XX
AC   ABC34321;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 34338 for detecting SNP TSC0010965.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 34338; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||||||||||
Db          1 CCCACCTTCTT 11


RESULT 8
ABC45614/c
ID   ABC45614 standard; DNA; 13 BP.
XX
AC   ABC45614;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 45631 for detecting SNP TSC0013272.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 45631; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
```

```
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||||||||||
Db         12 CCCACCTTCTT 2


RESULT 9
ABC45615
ID   ABC45615 standard; DNA; 13 BP.
XX
AC   ABC45615;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 45632 for detecting SNP TSC0013272.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 45632; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||||||||||
Db          2 CCCACCTTCTT 12


RESULT 10
AAZ81481/c
ID   AAZ81481 standard; DNA; 10 BP.
XX
AC   AAZ81481;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #715.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 77; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
```

```
SQ   Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 ACCTTCTTGG 13
              ||||||||||
Db         10 ACCTTCTTGG 1


RESULT 11
ABV70040
ID   ABV70040 standard; cDNA; 11 BP.
XX
AC   ABV70040;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7826.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 249; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTGGG 14
              ||||||||||
Db          1 CCTTCTTGGG 10


RESULT 12
ABV62619
ID   ABV62619 standard; cDNA; 11 BP.
XX
AC   ABV62619;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 405.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 37; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTGGG 14
              ||||||||||
Db          1 CCTTCTTGGG 10


RESULT 13
ABH76170
ID   ABH76170 standard; DNA; 12 BP.
XX
AC   ABH76170;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 276163 for detecting SNP TSC0004105.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 276163; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              ||||||||||
Db          1 CCACCTTCTT 10


RESULT 14
ABI71877
ID   ABI71877 standard; DNA; 12 BP.
XX
AC   ABI71877;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 371850 for detecting SNP TSC0059032.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 371850; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||||||
Db          2 CCCACCTTCT 11


RESULT 15
AAA54180/c
ID   AAA54180 standard; cDNA; 13 BP.
XX
AC   AAA54180;
XX
DT   08-FEB-2001  (first entry)
XX
DE   5' exon-intron junction of exon 3 of BSMAP.
XX
KW   Brain specific membrane anchored protein; BSMAP; dopamine; GABA;
KW   receptor; agonist; antagonist; central nervous system; CNS;
KW   brain disease; chromosome 19; CLF-I; depression; dyslexia; dystonia;
KW   eating disorder; epilepsy; migraine; headache; panic disorder;
KW   schizophrenia; obsessive disorder; compulsive disorder;
KW   amyotrophic lateral sclerosis; multiple sclerosis; Alzheimer's disease;
KW   brain tumour; Huntington's disease; Parkinson's disease; stroke; human;
KW   exon; intron; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055317-A1.
XX
PD   21-SEP-2000.
XX
PF   16-MAR-2000; 2000WO-IB000360.
XX
PR   16-MAR-1999;   99EP-00400636.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Elson G,  Bonnefoy J,  Gauchat J;
XX
DR   WPI; 2000-638200/61.
XX
PT   Novel nucleic acid encoding Brain-Specific Membrane Anchored Protein
PT   useful for treating central nervous system associated disorders and
PT   diseases.
XX
PS   Disclosure; Page 13; 45pp; English.
XX
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CC   Several receptors (dopamine receptors, the 5-HT family of receptors and
CC   GABA receptors) have been shown to be useful targets by agonist and
CC   antagonist compounds to treat and/or prevent CNS disorders. Brain
CC   receptors in general are attractive candidates for finding new therapies
CC   for brain diseases. Human chromosome 19 is a short chromosome with a
CC   relatively high GC content which has been found to be involved in CNS
CC   functions. The gene for type I cytokine receptor homologue CLF-1 was
CC   recently localised to chromosome 19. Unexpectedly seven other exons
CC   coding in the reverse orientation located adjacent to the CLF-1 exons
CC   have also been found. This new gene was designated brain-specific
CC   membrane anchored protein (BSMAP). Antagonistic compounds directed
CC   against BSMAP are useful for preparing medicaments for treating and/or
CC   preventing central nervous system disorders such as depression, dyslexia,
CC   dystonia, eating disorders, epilepsy, migraine, headache, panic disorder,
CC   schizophrenia, obsessive and compulsive disorders, amyotrophic lateral
CC   sclerosis, multiple sclerosis, Alzheimer's disease, brain tumors,
CC   Huntington's disease, Parkinson's disease and stroke
XX
SQ   Sequence 13 BP; 3 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||||||
Db         10 CCCACCTTCT 1


RESULT 16
ABC48640
ID   ABC48640 standard; DNA; 13 BP.
XX
AC   ABC48640;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 48657 for detecting SNP TSC0013839.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 48657; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 29;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TCTTGGGCAGAAG 20
              | ||||| |||||
Db          1 TTTTGGGTAGAAG 13


RESULT 17
ABC48641/c
ID   ABC48641 standard; DNA; 13 BP.
XX
AC   ABC48641;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 48658 for detecting SNP TSC0013839.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 48658; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 29;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TCTTGGGCAGAAG 20
              | ||||| |||||
```

```
Db         13 TTTTGGGTAGAAG 1


RESULT 18
ABF26997/c
ID   ABF26997 standard; DNA; 13 BP.
XX
AC   ABF26997;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 126994 for detecting SNP TSC0031788.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 126994; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 29;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCAGAA 19
              || ||||| ||||
Db         13 TTGTTGGGGAGAA 1


RESULT 19
ABF26996
ID   ABF26996 standard; DNA; 13 BP.
XX
AC   ABF26996;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 126993 for detecting SNP TSC0031788.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 126993; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 29;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCAGAA 19
              || ||||| ||||
Db          1 TTGTTGGGGAGAA 13


RESULT 20
ABK99486/c
ID   ABK99486 standard; DNA; 11 BP.
XX
AC   ABK99486;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human CYP3A5 gene polymorphic reference DNA sequence #56.
XX
KW   Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW   AIDS; African American; forensic marker; pharmacological; cytostatic;
KW   antidiabetic; anti-HIV; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200253775-A2.
XX
PD   11-JUL-2002.
XX
PF   21-DEC-2001; 2001WO-EP015290.
XX
PR   28-DEC-2000; 2000EP-00128627.
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PR 28-DEC-2000; 2000US-0258684P.
PR 29-DEC-2000; 2000US-0258952P.
PR 16-JAN-2001; 2001EP-00100172.
PR 18-JAN-2001; 2001US-0262859P.
PR 16-AUG-2001; 2001EP-00118884.
PR 16-AUG-2001; 2001US-0312825P.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Haberl M, Hustert E;
XX
DR WPI; 2002-583628/62.
XX
PT Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT cardiovascular diseases, diabetes and AIDS, and for identifying
PT polymorphisms.
XX
PS Example 2; Page 53; 138pp; English.
XX
CC The present invention relates to a new CYP3A5 polynucleotide encoding a
CC polypeptide, where the polynucleotide is capable of hybridising to a
CC CYP3A5 gene. The invention is useful in an in vitro method for
CC identifying a polymorphism. The invention is also useful for useful for
CC diagnosing a disorder related to the presence of a molecular variant of a
CC CYP3A5 or susceptibility to such a disorder, where the disorder is
CC cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC The invention can further be used for the preparation of a diagnostic
CC composition for diagnosing a disease in a subject having a genome
CC comprising a variant allele of the CYP3A5 gene, where the subject is an
CC African American. The molecules of the invention are as forensic markers
CC and in pharmacological studies. The present nucleic acid sequence
CC represents a human CYP3A5 gene polymorphism reference DNA sequence, as
CC described in the invention
XX
SQ Sequence 11 BP; 4 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TCTTGGGCAGA 18
||||.||||||
Db 11 TCTTTGGCAGA 1

RESULT 21
ABI13302
ID ABI13302 standard; DNA; 12 BP.
XX
AC ABI13302;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 313275 for detecting SNP TSC0025624.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 313275; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCACCTTCTT 11
|||||||||.|
Db 1 CCCACCTTCAT 11

RESULT 22
ABI47015/c
ID ABI47015 standard; DNA; 12 BP.
XX
AC ABI47015;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 346988 for detecting SNP TSC0044863.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 346988; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

```
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||||||||| |
Db         12 CCCACCTTCCT 2


RESULT 23
ABI45565/c
ID   ABI45565 standard; DNA; 12 BP.
XX
AC   ABI45565;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 345538 for detecting SNP TSC0044079.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 345538; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||||||| |||
Db         12 CCCACCTCCTT 2


RESULT 24
ABI69022/c
ID   ABI69022 standard; DNA; 12 BP.
XX
AC   ABI69022;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 368995 for detecting SNP TSC0057391.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 368995; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||||||| |||
Db         12 CCCACCTACTT 2


RESULT 25
ABH91427
ID   ABH91427 standard; DNA; 12 BP.
XX
AC   ABH91427;
XX
DT   22-FEB-2002  (first entry)
```

```
XX
DE   Oligonucleotide primer SEQ ID NO 291420 for detecting SNP TSC0014786.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 291420; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 5 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              || ||||||||
Db          1 CCTACCTTCTT 11


RESULT 26
ABI61189/c
ID   ABI61189 standard; DNA; 12 BP.
XX
AC   ABI61189;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 361162 for detecting SNP TSC0052480.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 361162; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAAG 20
              ||||| |||||
Db         12 TTGGGTAGAAG 2


RESULT 27
ABH98731
ID   ABH98731 standard; DNA; 12 BP.
XX
AC   ABH98731;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 298724 for detecting SNP TSC0018250.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
```

```
XX
PS   Claim 1; SEQ ID NO 298724; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              |||||||||  |
Db          1 CCCACCTTCCT 11


RESULT 28
ABH85586/c
ID   ABH85586 standard; DNA; 12 BP.
XX
AC   ABH85586;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 285579 for detecting SNP TSC0012359.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 285579; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCTT 11
              ||| |||||||
Db         12 CCCTCCTTCTT 2


RESULT 29
AAZ77982/c
ID   AAZ77982 standard; DNA; 10 BP.
XX
AC   AAZ77982;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:410.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
```

```
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 76; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db          9 CCCACCTTC 1


RESULT 30
AAZ78502/c
ID   AAZ78502 standard; DNA; 10 BP.
XX
AC   AAZ78502;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:930.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 92; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
```

```
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGGCAGAA 19
               |||||||||
Db          10 TGGGCAGAA 2


RESULT 31
AAZ78803/c
ID   AAZ78803 standard; DNA; 10 BP.
XX
AC   AAZ78803;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1231.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 100; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 CCACCTTCT 10
               |||||||||
Db          10 CCACCTTCT 2


RESULT 32
AAZ82426/c
ID   AAZ82426 standard; DNA; 10 BP.
XX
AC   AAZ82426;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1660.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
```

XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 103; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGGCAGAAG 20
|||||||||
Db 10 GGGCAGAAG 2

RESULT 33
AAF42275/c
ID AAF42275 standard; DNA; 10 BP.
XX
AC AAF42275;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9014.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 321; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCTTCTTG 12
|||||||||
Db 10 ACCTTCTTG 2

RESULT 34
ABT14287
ID ABT14287 standard; DNA; 10 BP.
XX
AC ABT14287;
XX
DT 20-FEB-2003 (first entry)
XX
DE Nucleic acid PCR amplification method-related RAPD PCR primer #57.
XX
KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS Unidentified.
XX
PN WO200281743-A2.

XX
PD 17-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-GB001489.
XX
PR 02-APR-2001; 2001GB-00008182.
XX
PA (HAMI/) HAMILL B.
XX
PI Hamill B;
XX
DR WPI; 2003-075484/07.
XX
PT Amplification of nucleotide sequences from polynucleotides by chain
PT extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT solution, 2 attached to supports and both share complementary sequences.
XX
PS Disclosure; Fig 17; 60pp; English.
XX
CC The invention comprises a method for the PCR amplification of nucleic
CC acids. The method involves a set of primers, where two of the primers are
CC in solution and at least two other primers are attached to a solid
CC support. The method of the invention can be used for the analysis of a
CC nucleic acid or a mixture of nucleic acids, including: single-stranded
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC PCR primer of the invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TCTTGGGCA 16
|||||||||
Db 2 TCTTGGGCA 10

RESULT 35
AAA87795
ID AAA87795 standard; DNA; 11 BP.
XX
AC AAA87795;
XX
DT 28-NOV-2000 (first entry)
XX
DE Promoter P15B3 transcription factor binding site SEQ ID #159.
XX
KW Human; secreted protein; forensic procedure; gene therapy;
KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
KW mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease;
KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KW septic shock; impotence; promoter; P15B3; ds.
XX
OS Homo sapiens.
XX
PN WO200037491-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-IB002058.
XX
PR 22-DEC-1998; 98US-0113686P.
PR 25-JUN-1999; 99US-0141032P.
XX
PA (GEST) GENSET.
XX
PI Bougueleret L, Dumas J, Duclert A;
XX
DR WPI; 2000-442637/38.
XX
PT Polynucleotides and polypeptides encoding proteins with signal peptides,
PT useful in diagnostic, forensic, gene therapy and chromosome mapping
PT procedures.
XX
PS Example 48; Fig 5; 306pp; English.
XX
CC This sequence represents a transcription factor binding site identified
CC in the human P15B3 promoter. The invention relates to sequences AAA87725-
CC A87774 which encode human secreted proteins AAB25763-B25812. The proteins
CC include signal peptides. The P15B3 promoter is used in the isolation of
CC the cDNAs of the invention. Included in the invention are a host cell
CC containing one of the cDNA sequences, and a purified antibody capable of
CC binding to one of the secreted proteins. Also contained in the invention
CC are methods for storing the sequence data on a computer system, and a
CC method for identifying features of the cDNA sequences using a computer
CC programme. The cDNAs are useful for expressing secreted proteins or
CC fragments to obtain antibodies capable of specifically binding to the
CC secreted proteins. The cDNAs may also be useful in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence
XX
SQ Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACCTTC 9
|||||||||
Db 2 CCCACCTTC 10

RESULT 36
AAS07926
ID AAS07926 standard; DNA; 11 BP.
XX
AC AAS07926;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human transcription factor binding site from promoter P15B4 #5.
XX
KW Human; expressed sequence tag; EST; ds; promoter P15B4;
KW acute myocardial infarction; acute ischaemic stroke; diabetes; anaemia;
KW growth hormone deficiency; hepatitis; kidney carcinoma;
KW multiple sclerosis; chemotherapy-induced neutropaenia;
KW transcription factor binding site.
XX
OS Homo sapiens.
XX
PN EP1104808-A1.
XX
PD 06-JUN-2001.
XX
PF 27-JUL-2000; 2000EP-00202699.
XX
PR 05-AUG-1999; 99US-0147499P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Jobert S, Giordano J;
XX
DR WPI; 2001-357986/38.
XX
PT New purified 5' expressed sequence tags useful in diagnostic, forensic,
PT gene therapy or chromosome mapping procedures, or for distinguishing

PT human tissues or cells from non-human tissues or cells.
XX
PS Example 53; Fig 5; 90pp; English.
XX
CC The sequence represents a transcription factor binding site from human
CC promoter P15B4, the promoter and binding site being isolated using
CC sequence from one of the 5' expressed sequence tags (EST) of the
CC invention, one of 15442 nucleotide sequences not given in the
CC specification. The 5' EST may be used to efficiently identify and isolate
CC 5'untranslated regions (UTRs) and upstream regulatory regions which
CC control the location, developmental stage, rate and quantity of protein
CC synthesis, as well as the stability of the mRNA. ESTs containing the 5'
CC ends of protein genes may include sequences for chromosome mapping and
CC identification individuals. The EST may further be used to distinguish
CC human tissues or cells from non-human tissues or cells, to distinguish
CC between human tissues or cells that do not and do not express
CC polynucleotides comprising the 5' EST sequences, to obtain and express
CC cDNA clones which include full protein coding sequences of the
CC corresponding gene products, to map and clone promoter regions, and open
CC reading frames from a genomic sequence, and to obtain and express
CC extended cDNAs encoding portions of the protein. EST-related nucleic
CC acids are useful in forensic procedures or in diagnosis of genetic
CC diseases resulting from abnormal gene expression, for constructing a high
CC resolution map of human chromosomes, and in gene therapy to control or
CC treat genetic diseases. Proteins expressed from the cDNAs may be used in
CC treating or controlling a variety of human conditions e.g acute
CC myocardial infarction, acute ischaemic stroke, diabetes, anaemia, growth
CC hormone deficiency, hepatitis, kidney carcinoma, multiple sclerosis,
CC chemotherapy-induced neutropaenia
XX
SQ Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

```
  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db          2 CCCACCTTC 10
```

RESULT 37
ABV64418
ID ABV64418 standard; cDNA; 11 BP.
XX
AC ABV64418;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2204.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 86; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

```
  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAAG 20
              |||||||||
Db          1 GGGCAGAAG 9
```

RESULT 38
ABV71839
ID ABV71839 standard; cDNA; 11 BP.
XX
AC ABV71839;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9625.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 311; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

```
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAAG 20
              |||||||||
Db          1 GGGCAGAAG 9


RESULT 39
AAK99270
ID   AAK99270 standard; DNA; 11 BP.
XX
AC   AAK99270;
XX
DT   31-MAY-2002  (first entry)
XX
DE   P15B4 promoter transcription binding site DELTAEF1_01.
XX
KW   Promoter DNA; diagnostic; forensic; gene therapy; chromosome mapping;
KW   expression vector; secretion vector; P15B4; transcription binding site;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   CA2343602-A1.
XX
PD   18-OCT-2001.
XX
PF   17-APR-2001; 2001CA-02343602.
XX
PR   18-APR-2000; 2000US-0197873P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards JB,  Jobert S,  Giordano J,  Tanaka H,  Bejanin S;
XX
DR   WPI; 2002-227459/29.
XX
PT   New nucleic acid sequences comprising human expressed sequence tags
PT   (ESTs), useful in diagnostic, forensic, gene therapy or chromosome
PT   mapping procedures, or for designing expression vectors and secretion
PT   vectors.
XX
PS   Disclosure; Fig 5; 163pp; English.
XX
CC   The invention relates to purified nucleic acids, which comprise sequences
CC   selected from any of more than 50000 sequences not defined in the
CC   specification. The polynucleotide sequences are useful in making cDNA,
CC   polypeptides and promoter DNA, and in diagnostic, forensic, gene therapy
CC   or chromosome mapping procedures. The nucleic acid sequences are also
CC   useful for designing expression vectors and secretion vectors. This
CC   polynucleotide sequence represents a P15B4 promoter transcription binding
CC   site of the invention
XX
SQ   Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db          2 CCCACCTTC 10


RESULT 40
AAS21210
ID   AAS21210 standard; DNA; 11 BP.
XX
AC   AAS21210;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transmissible gastroenteritis virus full length clone, C/DE-1 junction.
XX
KW   Transmissible gastroenteritis virus; TGE; gene transfer;
KW   recombinant viral genome; gene therapy; artificial chromosome; vaccine;
KW   ds.
XX
OS   Transmissible gastroenteritis virus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(6,T)
FT                   /*tag=  a
FT   misc_feature    7. .8
FT                   /*tag=  b
FT                   /label= Cleavage_site
FT                   /note= "Restriction enzyme Bgl1 cleaves at this site
FT                   creating a sticky end"
FT   mutation        replace(10,A)
FT                   /*tag=  c
XX
PN   WO200190340-A2.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-US016564.
XX
PR   21-MAY-2000; 2000US-0206537P.
PR   20-APR-2001; 2001US-0285320P.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Baric RS,  Yount B;
XX
DR   WPI; 2002-114288/15.
XX
PT   Directionally assembling a recombinant viral genome, useful for
PT   manipulating the genomes of plants, animals, bacteria or viruses for gene
PT   therapy, by ligating the subclones of the viral genome to assemble a
PT   recombinant viral genome.
XX
PS   Example 7; Page 22; 42pp; English.
XX
CC   The invention describes a method of directionally assembling a
CC   recombinant viral genome comprising ligating the subclones of the viral
CC   genome to assemble a recombinant viral genome, particularly coronavirus.
CC   For directionally assembling a recombinant viral genome. In particular,
CC   the method is useful for manipulating the genomes of higher plants and
CC   animals, as well as bacteria and viruses. In particular, the method is
CC   useful for the precise genetic manipulation of individual chromosomes in
CC   whole plants and animals and the construction of artificial chromosomes
CC   for gene therapy. The genomes produced are useful in preparing vaccines
CC   and expression vectors (e.g., TGE vectors and vaccines), which are useful
CC   in protocols involving vaccination, gene transfer and gene therapy. This
CC   sequence represents the interconnecting junction site C/DE-1 used in the
CC   assembly of the full length transmissible gastroenteritis virus (TGE)
CC   genome described in the method of the invention
XX
SQ   Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTGG 13
              |||||||||
Db          2 CCTTCTTGG 10
```

```
RESULT 41
ABI19388/c
ID   ABI19388 standard; DNA; 12 BP.
XX
AC   ABI19388;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 319361 for detecting SNP TSC0029179.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 319361; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTT 11
              |||||||||
Db          9 CACCTTCTT 1


RESULT 42
ABI08577/c
ID   ABI08577 standard; DNA; 12 BP.
XX
AC   ABI08577;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 308550 for detecting SNP TSC0023078.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 308550; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTT 11
              |||||||||
Db         10 CACCTTCTT 2


RESULT 43
ABI25588/c
ID   ABI25588 standard; DNA; 12 BP.
XX
AC   ABI25588;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 325561 for detecting SNP TSC0032603.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
```

```
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 325561; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTT 11
              |||||||||
Db         11 CACCTTCTT 3


RESULT 44
ABI13144/c
ID   ABI13144 standard; DNA; 12 BP.
XX
AC   ABI13144;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 313117 for detecting SNP TSC0025502.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 313117; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db         12 CCCACCTTC 4


RESULT 45
ABI48769
ID   ABI48769 standard; DNA; 12 BP.
XX
AC   ABI48769;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 348742 for detecting SNP TSC0045724.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 348742; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 7 C; 0 G; 4 T; 0 U; 0 Other;
```

```
  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db          4 CCCACCTTC 12


RESULT 46
ABH88612
ID   ABH88612 standard; DNA; 12 BP.
XX
AC   ABH88612;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 288605 for detecting SNP TSC0013593.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 288605; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTT 11
              |||||||||
Db          1 CACCTTCTT 9


RESULT 47
ABI67143/c
ID   ABI67143 standard; DNA; 12 BP.
XX
AC   ABI67143;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 367116 for detecting SNP TSC0056171.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 367116; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTT 11
              |||||||||
Db          9 CACCTTCTT 1


RESULT 48
ABH94365
ID   ABH94365 standard; DNA; 12 BP.
XX
AC   ABH94365;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 294358 for detecting SNP TSC0016077.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
```

PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 294358; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCACCTTCT 10
|||||||||
Db 4 CCACCTTCT 12

RESULT 49
ABH96358
ID ABH96358 standard; DNA; 12 BP.
XX
AC ABH96358;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 296351 for detecting SNP TSC0017041.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 296351; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACCTTC 9
|||||||||
Db 4 CCCACCTTC 12

RESULT 50
ABH74429/c
ID ABH74429 standard; DNA; 12 BP.
XX
AC ABH74429;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 274414 for detecting SNP TSC0003539.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 274414; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

```
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match            45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db         11 CCCACCTTC 3


RESULT 51
ABH70993/c
ID   ABH70993 standard; DNA; 12 BP.
XX
AC   ABH70993;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 270970 for detecting SNP TSC0002341.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 270970; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match            45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTC 9
              |||||||||
Db         11 CCCACCTTC 3


RESULT 52
ABH88613
ID   ABH88613 standard; DNA; 12 BP.
XX
AC   ABH88613;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 288606 for detecting SNP TSC0013593.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 288606; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match            45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTT 11
              |||||||||
Db          1 CACCTTCTT 9


RESULT 53
ABI52693
ID   ABI52693 standard; DNA; 12 BP.
XX
AC   ABI52693;
XX
DT   22-FEB-2002  (first entry)
XX
```

```
DE   Oligonucleotide primer SEQ ID NO 352666 for detecting SNP TSC0048025.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 352666; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCT 10
              |||||||||
Db          2 CCACCTTCT 10


RESULT 54
ABI40468/c
ID   ABI40468 standard; DNA; 12 BP.
XX
AC   ABI40468;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 340441 for detecting SNP TSC0041530.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 340441; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCT 10
              |||||||||
Db          9 CCACCTTCT 1


RESULT 55
ABI10163/c
ID   ABI10163 standard; DNA; 12 BP.
XX
AC   ABI10163;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 310136 for detecting SNP TSC0023830.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
```

```
PS   Claim 1; SEQ ID NO 310136; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCT 10
              |||||||||
Db         12 CCACCTTCT 4


RESULT 56
ABH94363
ID   ABH94363 standard; DNA; 12 BP.
XX
AC   ABH94363;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 294356 for detecting SNP TSC0016077.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 294356; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCT 10
              |||||||||
Db          4 CCACCTTCT 12


RESULT 57
ABI73341/c
ID   ABI73341 standard; DNA; 12 BP.
XX
AC   ABI73341;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 373314 for detecting SNP TSC0059971.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 373314; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCT 10
              |||||||||
Db          9 CCACCTTCT 1
```

```
RESULT 58
AAD25619
ID   AAD25619 standard; DNA; 12 BP.
XX
AC   AAD25619;
XX
DT   26-MAR-2002  (first entry)
XX
DE   MLLCy5L LNA probe used for haplotyping MLL-AF4/98(+) chimeric gene.
XX
KW   Haplotyping; single molecule detection; luminescent marker;
KW   genetic marker; MLL-AF4/98(+); locked nucleic acid; LNA; probe; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N,N'-biscarboxypentyl-5, 5'-
FT                   disulfonatoindodicarbocyanine (Cy5) fluorophore labelled
FT                   thymine"
XX
PN   WO200190418-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US016394.
XX
PR   22-MAY-2000; 2000US-0206512P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cai H,  Goodwin PM,  Keller RA,  Werner JH;
XX
DR   WPI; 2002-083123/11.
XX
PT   Rapid haplotyping of DNA or RNA segments, comprises labeling at least 2
PT   target sites on a segment of DNA or RNA with separate distinguishable
PT   luminescent hybridization probes.
XX
PS   Example 1; Page 22; 49pp; English.
XX
CC   The invention relates to rapid haplotyping a DNA or RNA segment by single
CC   molecule detection. The method involves labelling at least 2 target sites
CC   on a DNA or RNA segment with separate distinguishable luminescent marker
CC   hybridisation probes, where the targets are selected genetic markers and
CC   detecting the presence or absence of each luminescent hybridisation probe
CC   on each DNA segment to determine the haplotype of each DNA or RNA
CC   segment. The method is useful for rapid haplotyping of DNA or RNA
CC   segment. The present sequence is a locked nucleic acid (LNA) probe used
CC   for haplotyping MLL-AF4/98(+) chimeric gene
XX
SQ   Sequence 12 BP; 0 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGC 15
              |||||||||
Db          2 TTCTTGGGC 10


RESULT 59
AAD25617
ID   AAD25617 standard; DNA; 12 BP.
XX
AC   AAD25617;
XX
DT   26-MAR-2002  (first entry)
XX
DE   MLLCy5P PNA probe used for haplotyping MLL-AF4/98(+) chimeric gene.
XX
KW   Haplotyping; single molecule detection; luminescent marker;
KW   genetic marker; MLL-AF4/98(+); peptide nucleic acid; PNA; probe; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N,N'-biscarboxypentyl-5, 5'-
FT                   disulfonatoindodicarbocyanine (Cy5) fluorophore labelled
FT                   thymine; This base is linked to the label via linker"
FT   misc_feature    12
FT                   /*tag=  b
FT                   /note= "This base is attached to a linker sequence"
XX
PN   WO200190418-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US016394.
XX
PR   22-MAY-2000; 2000US-0206512P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cai H,  Goodwin PM,  Keller RA,  Werner JH;
XX
DR   WPI; 2002-083123/11.
XX
PT   Rapid haplotyping of DNA or RNA segments, comprises labeling at least 2
PT   target sites on a segment of DNA or RNA with separate distinguishable
PT   luminescent hybridization probes.
XX
PS   Example 1; Page 22; 49pp; English.
XX
CC   The invention relates to rapid haplotyping a DNA or RNA segment by single
CC   molecule detection. The method involves labelling at least 2 target sites
CC   on a DNA or RNA segment with separate distinguishable luminescent marker
CC   hybridisation probes, where the targets are selected genetic markers and
CC   detecting the presence or absence of each luminescent hybridisation probe
CC   on each DNA segment to determine the haplotype of each DNA or RNA
CC   segment. The method is useful for rapid haplotyping of DNA or RNA
CC   segment. The present sequence is a peptide nucleic acid (PNA) probe used
CC   for haplotyping MLL-AF4/98(+) chimeric gene
XX
SQ   Sequence 12 BP; 0 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGC 15
              |||||||||
Db          2 TTCTTGGGC 10


RESULT 60
AAT14161/c
ID   AAT14161 standard; DNA; 10 BP.
XX
AC   AAT14161;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
```

XX
PN WO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US004477.
XX
PR 14-APR-1994; 94US-00228935.
PR 27-MAR-1995; 95US-00410780.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Seidel HM, Lamb IP;
XX
DR WPI; 1995-373797/48.
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for detecting
PT the presence of transcriptional regulatory protein in a sample.
XX
PS Claim 7; Page 125; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element TT(Nx)AA,
CC where x is 4-7, and the regulatory element binds an activated
CC transcriptional regulatory protein in response to a signalling mol., i.e.
CC a cytokine. This cytokine responsive DNA spacer regulatory element can be
CC used to detect the presence of a transcriptional regulatory protein in a
CC sample, and in assays for (ant)agonists of gene transcription. The
CC identified cpds. may be used to treat cytokine-induced disease states, or
CC to ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions
XX
SQ Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TTCTTGGGCA 16
||||||||| |
Db 10 TTCTTGGGAA 1

RESULT 61
AAV56888/c
ID AAV56888 standard; DNA; 10 BP.
XX
AC AAV56888;
XX
DT 02-DEC-1998 (first entry)
XX
DE Regulatory element containing oligonucleotide #47.
XX
KW Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW transcriptional control; STAT protein; screening; agonist; ss.
XX
OS Synthetic.
XX
PN US5814517-A.
XX
PD 29-SEP-1998.
XX
PF 27-MAR-1995; 95US-00410779.
XX
PR 14-APR-1994; 94US-00228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;
XX
DR WPI; 1998-541763/46.
XX
PT DNA constructs containing cytokine-responsive regulatory elements -
PT useful in assays for transcription-regulating proteins or gene
PT transcription agonists or antagonists.
XX
PS Disclosure; Col 12; 58pp; English.
XX
CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
CC production of constructs comprising a cytokine-responsive regulatory
CC element linked to a promoter which is linked to a heterologous coding
CC sequence so that the coding sequence is under the transcriptional control
CC of the regulatory element and the promoter, where the regulatory element
CC has a nucleotide sequence selected from TTCNNGAA, TTANyTAA, and TTCNyTAA
CC where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,
CC in a sample by contacting the sample with the construct so that the
CC protein binds to the regulatory element, and detecting or separating the
CC resulting complex. The cells can be used in screening assays for agonists
CC of gene transcription, in which the level of expression of the coding
CC sequence is measured in the presence and absence of a test compound or in
CC the presence of the corresponding cytokine
XX
SQ Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TTCTTGGGCA 16
||||||||| |
Db 10 TTCTTGGGAA 1

RESULT 62
AAZ79653/c
ID AAZ79653 standard; DNA; 10 BP.
XX
AC AAZ79653;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:2081.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.

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PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 124; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              |||||| |||
Db         10 CCCACCCTCT 1


RESULT 63
AAZ77834
ID   AAZ77834 standard; DNA; 10 BP.
XX
AC   AAZ77834;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:262.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 71; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
```

```
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              | ||||||||
Db          1 TGCTTGGGCA 10


RESULT 64
AAZ78009
ID   AAZ78009 standard; DNA; 10 BP.
XX
AC   AAZ78009;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:437.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 77; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||||| |||
Db          1 CCACCTGCTT 10


RESULT 65
AAZ84938/c
ID   AAZ84938 standard; DNA; 10 BP.
XX
AC   AAZ84938;
```

```
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4172.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 170; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 66
AAZ85708
ID   AAZ85708 standard; DNA; 10 BP.
XX
AC   AAZ85708;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4942.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 190; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              || |||||||
Db          1 CTGCTTGGGC 10


RESULT 67
```

```
AAZ81181
ID   AAZ81181 standard; DNA; 10 BP.
XX
AC   AAZ81181;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #415.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 69; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TCTTGGGCAG 17
              | ||||||||
Db          1 TTTTGGGCAG 10
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```
RESULT 68
AAZ80869
ID   AAZ80869 standard; DNA; 10 BP.
XX
AC   AAZ80869;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #103.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 61; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||| ||||||
```

```
Db          1 CCCCCCTTCT 10


RESULT 69
AAZ79893
ID   AAZ79893 standard; DNA; 10 BP.
XX
AC   AAZ79893;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell preferentially expressed SAGE tag, SEQ ID NO:184.
XX
KW   SAGE tag; serial analysis of gene expression; diagnosis;
KW   differential gene expression; characterisation; targetted expression;
KW   tumour; cancer; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966303-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-US013820.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106132/09.
XX
PT   New polynucleotide useful in cancer immunotherapy.
XX
PS   Claim 1; Page 62; 97pp; English.
XX
CC   Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts which are
CC   differentially expressed in a variety of normal or malignant cell types.
CC   Some of the transcripts correspond to known genes or ESTs (expressed
CC   sequence tags) which were previously unknown to be preferentially or
CC   differentially expressed in that particular cell type, while other
CC   transcripts correspond to novel genes. The invention also provides a
CC   nucleotide comprising a promoter sequence derived from one of the
CC   differentially expressed genes, which may optionally be operably linked
CC   to a foreign nucleotide sequence, and gene delivery vehicles and host
CC   cells comprising the polynucleotides of the invention. A nucleotide
CC   comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures
CC   to characterise a cell of a specific tissue type and to determine whether
CC   it is normal or malignant. They may be used to screen for agents that
CC   modulate expression of differentially expressed genes compound. The
CC   promoter/foreign gene construct of the invention may be used for
CC   targetted expression of the foreign gene in a particular cell type. For
CC   example, a promoter derived from a gene preferentially expressed in
CC   dendritic cells (antigen-presenting cells, or APCs), may be operably
CC   linked to a sequence encoding an immunostimulatory molecule and a
CC   sequence encoding an antigen. Such a construct could be transduced into
CC   APCs and would be useful for inducing an immune response by educating
CC   immune effector cells in vivo, or in cancer immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              | ||||||||
Db          1 TGCTTGGGCA 10


RESULT 70
AAA73656/c
ID   AAA73656 standard; DNA; 10 BP.
XX
AC   AAA73656;
XX
DT   30-JAN-2001  (first entry)
XX
DE   Probe #25 for sequencing by hybridisation.
XX
KW   Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200040758-A2.
XX
PD   13-JUL-2000.
XX
PF   06-JAN-2000; 2000WO-US000458.
XX
PR   06-JAN-1999;   99US-0115284P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac R,  Drmanac S,  Kita D,  Cooke C,  Xu C;
XX
DR   WPI; 2000-475839/41.
XX
PT   Identifying one or more sequences of a target nucleic acid (NA), useful
PT   for parallel analyses, comprises contacting the NA with a set of pools of
PT   probes comprising mixture of probes with different information regions.
XX
PS   Disclosure; Page 53; 196pp; English.
XX
CC   The present sequence is a probe used to demonstrate the method of the
CC   invention, which is concerned with the use of pools of probes to enable
CC   sequencing by hybridisation, a process known as SBH. Overlapping probes
CC   are used which allows the identification of sequences longer then the
CC   probe length, and either the target nucleic acid or the probe is
CC   labelled. The method of the invention is useful for assembling sequences
CC   and in parallel analyses
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CTTGGGCAGA 18
              |||||| |||
Db         10 CTTGGGGAGA 1


RESULT 71
AAH63873/c
ID   AAH63873 standard; cDNA; 10 BP.
XX
AC   AAH63873;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 713.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 55; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 72
AAF43792
ID   AAF43792 standard; DNA; 10 BP.
XX
AC   AAF43792;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11931.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 376; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              ||||| ||||
Db          1 TTGGGTAGAA 10


RESULT 73
AAF34723/c
ID   AAF34723 standard; DNA; 10 BP.
XX
AC   AAF34723;
XX
```

```
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1462.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 52; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ACCTTCTTGG 13
              |||||||| |
Db         10 ACCTTCTTAG 1


RESULT 74
AAF38664/c
ID   AAF38664 standard; DNA; 10 BP.
XX
AC   AAF38664;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5403.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 193; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              ||||||| ||
Db         10 CCACCTTGTT 1
```

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RESULT 75
AAF37520/c
ID   AAF37520 standard; DNA; 10 BP.
XX
AC   AAF37520;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4259.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 152; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TCTTGGGCAG 17
              |||| |||||
Db          10 TCTTCGGCAG 1


RESULT 76
AAF37547/c
ID   AAF37547 standard; DNA; 10 BP.
XX
AC   AAF37547;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4286.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 153; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          11 TGGGCAGAAG 20
               ||||| ||||
Db          10 TGGGCTGAAG 1
```

RESULT 77
AAF40919
ID AAF40919 standard; DNA; 10 BP.
XX
AC AAF40919;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7658.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 273; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| |
Db          1 CCCACCTTAT 10
```

RESULT 78
AAF38830/c
ID AAF38830 standard; DNA; 10 BP.
XX
AC AAF38830;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5569.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 198; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

```
XX
SQ   Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||| |||||
Db         10 CCACATTCTT 1


RESULT 79
AAF41899/c
ID   AAF41899 standard; DNA; 10 BP.
XX
AC   AAF41899;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8638.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 308; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| |
Db         10 CTTCTTGGTC 1


RESULT 80
AAF40814/c
ID   AAF40814 standard; DNA; 10 BP.
XX
AC   AAF40814;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7553.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 269; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
```

CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACCTTCTTGG 13
| ||||||||
Db 10 AACTTCTTGG 1

RESULT 81
ABL88354/c
ID ABL88354 standard; DNA; 10 BP.
XX
AC ABL88354;
XX
DT 20-MAY-2002 (first entry)
XX
DE Human CHRNE gene polymorphism detection primer, SEQ ID NO:88.
XX
KW Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNE;
KW chromosome 17p13-12; acetylcholine receptor; AChR;
KW neuromuscular junction; skeletal muscle; postnatal development;
KW congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;
KW genetic variant; single nucleotide polymorphism; SNP; gene therapy;
KW drug screening; primer extension; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200198316-A2.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-US019835.
XX
PR 20-JUN-2000; 2000US-0212870P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Amaro E, Bieglecki KM, Kliem SE, Koshy B, Tanguay DA;
XX
DR WPI; 2002-130787/17.
XX
PT Novel genetic variants of cholinergic receptor, nicotinic, epsilon
PT polypeptide gene useful in studying expression and function of the
PT protein, and for screening drugs to treat diseases e.g. congential
PT myasthenic syndrome.
XX
PS Claim 19; Page 15; 104pp; English.
XX
CC The invention relates to a method for haplotyping the cholinergic
CC receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an
CC individual, and also describes 17 novel polymorphic sites within the
CC human CHRNE gene. The CHRNE gene is located on chromosome 17p13-12 and
CC contains 12 exons which encode a 493 amino acid protein (ABB49112). The
CC CHRNE protein is one of the 5 subunits of mammalian acetylcholine
CC receptors (AChRs) found at neuromuscular junctions in juveniles and
CC adults, and is essential for the normal postnatal development of skeletal
CC muscle. Mutations in the CHRNE gene are associated with congenital
CC myasthenic syndrome (CMS). CHRNE gene sequences can therefore be used in
CC gene therapy. The CHRNE gene is also useful for studying the expression
CC and function of CHRNE, and in expressing CHRNE protein for use in
CC screening for candidate drugs to treat diseases related to CHRNE. The
CC method of the invention is useful for haplotyping the CHRNE gene in an
CC individual, and can also be used in pharmaceutical research to validate
CC CHRNE as a candidate target for, and in design of clinical trials of
CC candidate drugs for, treating a specific condition drugs or disease
CC predicted to be associated with CHRNE activity such as CMS. Polymorphisms
CC in the target region may be determined by the use of allele-specific
CC oligonucleotides (ASOs; ABL88370-ABL88320) as probes and primers, and by
CC primer extension using oligonucleotide primers comprising sequences
CC ABL88371-ABL88354. The CHRNE protein is useful for improving the
CC efficiency and reliability of several steps in the discovery and
CC development of drugs for treating diseases associated with CHRNE
CC activity, and may be used to screen drugs which target CHRNE. Sequences
CC ABL88321-ABL88354 represent sequences that are specifically claimed as
CC components of primers used to detect polymorphisms in the CHRNE gene by
CC primer extension
XX
SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCACCTTCT 10
||||| ||||
Db 10 CCCACGTTCT 1

RESULT 82
ABK37010
ID ABK37010 standard; DNA; 10 BP.
XX
AC ABK37010;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human ALAS2 gene allele-specific oligonucleotide PCR primer #9.
XX
KW Human; aminolevulinate delta synthase 2; ALAS2; haplotyping; primer; ss;
KW haplotype pair; single nucleotide polymorphism; genotyping; antianaemic;
KW gene therapy; drug screening; X-linked sideroblastic anaemia; sequencing;
KW hypochromic anaemia; probe; PCR.
XX
OS Homo sapiens.
XX
PN WO200210454-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US023914.
XX
PR 28-JUL-2000; 2000US-0221827P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Koshy B, Kliem S, Stephens JC;
XX
DR WPI; 2002-188755/24.
XX
PT New isolated human aminolevulinate delta synthase 2 polynucleotide,
PT useful for therapeutic purposes, for studying the expression and function
PT of the polynucleotide, and for expressing the aminolevulinate protein.
XX
PS Claim 18; Page 14; 90pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding human aminolevulinate delta synthase 2 (ALAS2). A method for
CC haplotyping the ALAS2 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the ALAS2 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the ALAS2 gene can be
CC identified by comparing the frequency of the haplotype or haplotype pair
CC in a population exhibiting the trait with the frequency of the haplotype

CC or haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. ALAS2 and its corresponding DNA are used
CC for studying the expression and function of ALAS2, for use in screening
CC for candidate drugs to treat diseases related to ALAS2 activity, such as
CC X-linked sideroblastic anaemia and hypochromic anaemia. The sequences are
CC also useful for studying the effect of variation on the biological
CC activity of ALAS2 as well as on the binding affinity of candidate drugs
CC targeting ALAS2. Sequences ABK36963-ABK37027 represent allele-specific
CC oligonucleotide probes, sequencing primers and PCR primers used to detect
CC ALAS2 gene polymorphisms
XX
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTTCTTGGGC 15
| |||||||||
Db 1 CATCTTGGGC 10

RESULT 83
ABL39516/c
ID ABL39516 standard; DNA; 10 BP.
XX
AC ABL39516;
XX
DT 22-APR-2002 (first entry)
XX
DE Human ETFB primer-extension oligonucleotide 22.
XX
KW Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO200202580-A2.
XX
PD 10-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US021306.
XX
PR 05-JUL-2000; 2000US-0215984P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
XX
DR WPI; 2002-154722/20.
XX
PT Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT useful for therapeutic purposes, for studying the expression and function
PT of the polynucleotide, and for expressing the flavoprotein.
XX
PS Claim 19; Page 15; 143pp; English.
XX
CC The invention comprises DNA, cDNA and protein sequences of the human
CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC chromosome 19q13.3-13.4). The invention specifically relates to the
CC identification of 27 novel polymorphic sites within the ETFB gene.
CC Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC for nine primary flavoprotein dehydrogenases and is located in the
CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC GAII. The novel ETFB polymorphisms identified in the invention are useful
CC for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC protein and nucleic acids of the invention are useful for studying the
CC expression and function of ETFB in vivo. The ETFB protein and nucleic
CC acids are also useful for testing the efficacy of therapeutic agents and
CC compounds for glutaric acidaemia type II. The nucleic acids of the
CC invention are useful in the production of a transgenic animal expressing
CC the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC represent claimed ETFB primer-extension oligonucleotides
XX
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TCTTGGGCAG 17
||||||| ||
Db 10 TCTTGGGGAG 1

RESULT 84
ABL52253
ID ABL52253 standard; DNA; 10 BP.
XX
AC ABL52253;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human PHKG2 preferred oligonucleotide primer SEQ ID NO:40.
XX
KW Human; phosphorylase kinase gamma 2 (testis); PHKG2; enzyme; SNP;
KW phosphorylase kinase gamma 2; single nucleotide polymorphism;
KW polymorphic; hepatotropic; gene therapy; glycogen storage disease;
KW liver cirrhosis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200194365-A2.
XX
PD 13-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US018814.
XX
PR 09-JUN-2000; 2000US-0210568P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Koshy B, Sanchis A, Sausker EA;
XX
DR WPI; 2002-404359/43.
XX
PT New variants of phosphorylase kinase gamma 2 isogenes, useful for
PT improving efficiency and reliability in the development of drugs for
PT treating diseases e.g. liver cirrhosis.
XX
PS Claim 18; Page 14; 76pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) comprising
CC a nucleotide sequence which is a polymorphic variant of a reference
CC sequence for human phosphorylase kinase gamma2 (testis) (PHKG2) gene or
CC its fragment, or a polymorphic variant of a reference sequence for a
CC PHKG2 cDNA or its fragment. Also described is an isolated polypeptide
CC (II) comprising an amino acid sequence which is a polymorphic variant of
CC a reference sequence for PHKG2 protein or its fragment, where the
CC reference sequence comprises a sequence (see ABB09290) of 406 amino
CC acids, and the polymorphic variant comprises one or more variant amino
CC acids selected from glutamic acid at a position corresponding to amino
CC acid position 153 and tryptophan at position corresponding to amino acid
CC position 329. (I) has hepatotropic activity and can be used in gene
CC therapy. (II) is useful in screening for drugs targeting (II), by
CC contacting a PHKG2 polymorphic variant with a candidate agent and

```
CC   assaying for binding activity. The identified candidate agents targeting
CC   PHKG2, are useful for treating liver cirrhosis and glycogen storage
CC   diseases. The present sequence represents a preferred oligonucleotide
CC   primer for the PHKG2 gene, which is used in the exemplification of the
CC   present invention
XX
SQ   Sequence 10 BP; 1 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db          1 CCCACCTCCT 10


RESULT 85
ABL52252/c
ID   ABL52252 standard; DNA; 10 BP.
XX
AC   ABL52252;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human PHKG2 preferred oligonucleotide primer SEQ ID NO:39.
XX
KW   Human; phosphorylase kinase gamma 2 (testis); PHKG2; enzyme; SNP;
KW   phosphorylase kinase gamma 2; single nucleotide polymorphism;
KW   polymorphic; hepatotropic; gene therapy; glycogen storage disease;
KW   liver cirrhosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200194365-A2.
XX
PD   13-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US018814.
XX
PR   09-JUN-2000; 2000US-0210568P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Koshy B,  Sanchis A,  Sausker EA;
XX
DR   WPI; 2002-404359/43.
XX
PT   New variants of phosphorylase kinase gamma 2 isogenes, useful for
PT   improving efficiency and reliability in the development of drugs for
PT   treating diseases e.g. liver cirrhosis.
XX
PS   Claim 18; Page 14; 76pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) comprising
CC   a nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for human phosphorylase kinase gamma2 (testis) (PHKG2) gene or
CC   its fragment, or a polymorphic variant of a reference sequence for a
CC   PHKG2 cDNA or its fragment. Also described is an isolated polypeptide
CC   (II) comprising an amino acid sequence which is a polymorphic variant of
CC   a reference sequence for PHKG2 protein or its fragment, where the
CC   reference sequence comprises a sequence (see ABB09290) of 406 amino
CC   acids, and the polymorphic variant comprises one or more variant amino
CC   acids selected from glutamic acid at a position corresponding to amino
CC   acid position 153 and tryptophan at position corresponding to amino acid
CC   position 329. (I) has hepatotropic activity and can be used in gene
CC   therapy. (II) is useful in screening for drugs targeting (II), by
CC   contacting a PHKG2 polymorphic variant with a candidate agent and
CC   assaying for binding activity. The identified candidate agents targeting
CC   PHKG2, are useful for treating liver cirrhosis and glycogen storage
CC   diseases. The present sequence represents a preferred oligonucleotide
CC   primer for the PHKG2 gene, which is used in the exemplification of the
CC   present invention
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTCCT 1


RESULT 86
ABV78454
ID   ABV78454 standard; cDNA; 10 BP.
XX
AC   ABV78454;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human transcription factor CA150 SAGE tag, SEQ ID NO:165.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   preferential expression; immune disorder; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002186482-A.
XX
PD   02-JUL-2002.
XX
PF   19-DEC-2000; 2000JP-00385816.
XX
PR   19-DEC-2000; 2000JP-00385816.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-594261/64.
XX
PT   Human activated Th1 and Th2 cell expression gene group, useful for the
PT   diagnosis and treatment of Th1 and Th2-related diseases.
XX
PS   Claim 19; Page 11; 60pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are expressed in activated human Th1
CC   and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC   of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC   lying nearest to the polyA region of cDNAs derived from a variety of
CC   genes. These tags serve to uniquely identify each transcript and can thus
CC   be used to analyse the pattern of gene expression in particular cell
CC   types. The invention also relates to proteins encoded by the genes
CC   expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC   inhibitors of the expression of groups of genes that are expressed in
CC   either or both the two cell types. Groups of genes expressed in Th1
CC   and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC   and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC   representing 171 genes which are more highly expressed in Th1 cells
CC   compared with Th2 cells
XX
SQ   Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              |||| |||||
Db          1 TTGGCCAGAA 10


RESULT 87
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```
ABV84246/c
ID   ABV84246 standard; cDNA; 10 BP.
XX
AC   ABV84246;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human mitochondrial F0 complex ATP synthase-like EST SAGE tag #56.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; EST; expressed sequence tag;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 1; Page 11; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84191-ABV84290 are SAGE tags representing the 100 most highly
CC   expressed genes out of those genes which are overexpressed in chronic
CC   hepatitis C liver tissue compared with normal liver tissue
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 88
ABK23703/c
ID   ABK23703 standard; DNA; 10 BP.
XX
AC   ABK23703;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #292 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGC 15
              ||||||| ||
Db         10 CTTCTTGTGC 1


RESULT 89
ABN84506
ID   ABN84506 standard; DNA; 10 BP.
XX
AC   ABN84506;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Rat smooth muscle myosin heavy chain gene CArG2 motif.
XX
KW   Smooth muscle; myosin; SM-MHC; rat; gene therapy; promoter; CArG2;
KW   antiarteriosclerotic; antiasthmatic; antiinflammatory; cardiant;
KW   hypotensive; transgenic animal; ds.
XX
OS   Rattus sp.
XX
PN   WO200259270-A2.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-US002016.
XX
```

PR 24-JAN-2001; 2001US-0263811P.
XX
PA (OWEN/) OWENS G K.
PA (MANA/) MANABE I.
XX
PI Owens GK, Manabe I;
XX
DR WPI; 2002-599772/64.
XX
PT New smooth muscle myosin heavy chain promoter/enhancers, useful for
PT smooth muscle tissue-specific targeting and expression, or for genetic
PT engineering as a means to investigate smooth muscle cell physiology and
PT pathophysiology.
XX
PS Example 4; Page 56; 110pp; English.
XX
CC The present sequence is the CArG2 motif of the promoter/enhancer region
CC of the rat smooth muscle myosin heavy chain (SM-MHC) gene (see also
CC ABN84504). The present invention provides polynucleotide sequences which
CC confer to an operably linked polynucleotide cell-specific expression
CC within SM cells in vivo. These are derived from the rat or human SM-MHC
CC gene. In some, the CArG2 or the intron CArG motif is mutated to confer
CC subtype specificity. For example, the present sequence is preferably
CC altered to the sequence given in ABN84507 by site-directed mutagenesis.
CC The heterologous polynucleotide linked to the SM-MHC promoter preferably
CC encodes a toxin, a prodrug-converting enzyme, a tumour suppressor, a
CC sensitising agent, an apoptotic factor, an angiogenesis inhibitor, a
CC cytokine or an immunogenic antigen, or is an antisense polynucleotide or
CC a catalytic polynucleotide. Expression vectors, e.g. retroviral, adeno-
CC associated viral and adenoviral vectors, host cells and transgenic
CC animals are provided. The SM-MHC promoter/enhancer provides for specific
CC expression in SM cells of the bladder, gastrointestinal tract or urinary
CC tract, aorta artery, carotid artery, pulmonary artery, vena cava vein or
CC vascular SM. The compositions and methods for targeted gene delivery and
CC expression are useful in treating diseases associated with abnormal
CC function of SM cells, e.g. systemic hypertension, pulmonary hypertension,
CC atherosclerosis, asthma, coronary artery disease, gastrointestinal
CC abnormalities, reproductive dysfunction or chronic bronchitis
XX
SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCTTCTTGGG 14
|||| |||||
Db 1 CCTTTTTGGG 10

RESULT 90
ACA60848
ID ACA60848 standard; DNA; 10 BP.
XX
AC ACA60848;
XX
DT 03-JUL-2003 (first entry)
XX
DE Rat smooth muscle myosin heavy chain wild-type CArG2 motif.
XX
KW Rat; ds; smooth muscle; myosin heavy chain; SM-MHC; CArG; hypotensive;
KW antiatherosclerotic; antiasthmatic; antiinflammatory; promoter; enhancer;
KW systemic hypertension; pulmonary hypertension; atherosclerosis; asthma;
KW coronary artery disease; gastrointestinal abnormality; stem cell;
KW reproductive dysfunction; chronic bronchitis; tissue regeneration.
XX
OS Rattus sp.
XX
PN US2003017549-A1.
XX
PD 23-JAN-2003.
XX
PF 24-JAN-2002; 2002US-00057726.
XX
PR 16-JAN-1998; 98US-0071300P.
PR 15-JAN-1999; 99WO-US001038.
PR 13-JUL-2000; 2000US-00600319.
PR 24-JAN-2001; 2001US-0263811P.
XX
PA (OWEN/) OWENS G K.
XX
PI Owens GK, Manabe I;
XX
DR WPI; 2002-599772/64.
XX
PT New smooth muscle myosin heavy chain promoter/enhancers, useful for
PT smooth muscle tissue-specific targeting and expression, or for genetic
PT engineering as a means to investigate smooth muscle cell physiology and
PT pathophysiology.
XX
PS Example 4; Page 23; 75pp; English.
XX
CC The invention relates to an isolated, synthetic, or recombinant
CC polynucleotide comprising a smooth muscle myosin heavy chain (SM-MHC)
CC promoter/enhancer sequence capable of conferring smooth muscle specific
CC expression in vivo. Also included are expression vectors comprising the
CC SM-MHC promoter/enhancers, a genetically engineered host cell comprising
CC the vector, a transgenic non-human animal comprising the SM-MHC promoter/
CC enhancer and screening a compound that modulates the activity of an SM-
CC MHC promoter/enhancer. The SM-MHC promoter/enhancer is useful for
CC expressing a polynucleotide (a reporter gene or polynucleotide encoding a
CC therapeutic protein) in a smooth muscle cell in vivo. The smooth muscle
CC cell is in a coronary artery, aorta, airway smooth muscle, or pulmonary
CC vascular smooth muscle, or bladder smooth muscle, gastrointestinal tract
CC smooth muscle, urinary tract smooth muscle, or gastrointestinal tract
CC smooth muscle, urinary tract smooth muscle, airway smooth muscle, vein
CC smooth muscle, or small branching artery smooth muscle. The SM-MHC
CC promoter/enhancer further comprises a minimal thymidine kinase (TK)
CC promoter. The targeted delivery of the SM-MHC promoter/enhancer is useful
CC for development of animal models of human disease to assist in
CC development of new therapeutic targets or development of animals models
CC for purpose of screening new drugs/therapies. The SM-MHC promoter/
CC enhancer facilitates targeted gene delivery to express a gene of interest
CC within an SMC. Targeted gene delivery and expression of the SM-MHC
CC promoter/enhancer is useful for treating diseases associated with
CC abnormal function of SMC including systemic hypertension, pulmonary
CC hypertension, atherosclerosis, asthma, coronary artery disease,
CC gastrointestinal abnormalities, reproductive dysfunction and chronic
CC bronchitis. The SM-MHC promoter/enhancer and transformed cells are useful
CC for identifying and selecting SMC derived from multi-potent stem cell
CC populations for purposes of tissue generation/regeneration for surgery
CC (e.g. for blood vessel, bladder, or gastrointestinal smooth muscle tissue
CC augmentation-reconstitution). The SM-MHC genes contain CArG motifs in
CC their promoter and first intron regions, these motifs are thought to be
CC responsible for smooth muscle cell subtype specific expression of SM-MHC.
CC The present sequence is a rat SM-MHC wild-type CArG motif
XX
SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCTTCTTGGG 14
|||| |||||
Db 1 CCTTTTTGGG 10

RESULT 91
ABQ72900
ID ABQ72900 standard; DNA; 10 BP.
XX
AC ABQ72900;
XX
DT 06-SEP-2002 (first entry)
XX

DE Human GRM8 gene polymorphism detection primer, SEQ ID NO:104.
XX
KW Human; glutamate receptor metabotropic 8; GRM8; receptor;
KW chromosome 7q31.3-32.1; neurotransmission; glutamate-mediated;
KW Smith-Lemli-Opitz syndrome; retinitis pigmentosa;
KW neuropathological disorder; neuroprotective; ophthalmological;
KW gene therapy; haplotyping; genotyping; haplotype; genetic variant;
KW single nucleotide polymorphism; SNP; drug screening; drug discovery;
KW primer extension; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200238587-A2.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-US047325.
XX
PR 09-NOV-2000; 2000US-0247576P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Chew A, Choi JY, Koshy B, Parks KE;
XX
DR WPI; 2002-519291/55.
XX
PT Genetic variants of Glutamate Receptor, Metabotropic 8 isogenes, useful
PT for improving efficiency and reliability in drug development for treating
PT neuropathological conditions and retinitis pigmentosa.
XX
PS Claim 17; Page 15; 110pp; English.
XX
CC The invention relates to a method for haplotyping the glutamate receptor,
CC metabotropic 8 (GRM8) gene (ABQ72798, ABQ72905) of an individual, and
CC also describes 21 novel polymorphic sites within the human GRM8 gene. The
CC GRM8 gene is located on chromosome 7q31.3-32.1 and contains 10 exons
CC which encode a 908 amino acid protein (ABB09564). GRM8 is involved in
CC glutamate-mediated neurotransmission, being a member of a subfamily of
CC metabotropic glutamate receptors that inhibit the activity of adenylate
CC cyclase in response to glutamate stimulation. The chromosomal location of
CC the GRM8 gene encompasses regions linked to Smith-Lemli-Opitz syndrome
CC and a form of retinitis pigmentosa. GRM8 nucleic acid sequences are
CC useful in studying the expression and function of GRM8, and in expressing
CC GRM8 protein for use in screening drugs for the treatment of GRM8-
CC associated diseases (e.g., neuropathological disorders, Smith-Lemli-Opitz
CC syndrome and retinitis pigmentosa). GRM8 nucleic acids and proteins are
CC also useful in studying the effect of polymorphisms on the biological
CC activity of GRM8. Polymorphisms in the target region may be determined by
CC the use of allele-specific oligonucleotides (ASOs; ABQ72800-ABQ72862) as
CC probes and primers, and by primer extension using oligonucleotide primers
CC comprising sequences ABQ72863-ABQ72904. The method of the invention is
CC useful for haplotyping the GRM8 gene in populations and in individuals,
CC enabling decisions to be made as to whether GRM8 is a likely therapeutic
CC target for a disease of interest, and in the design of clinical trials of
CC candidate drugs for treating GRM8-associated disorders. In addition,
CC transgenic animals comprising a human GRM8 gene are useful for studying
CC the expression of GRM8 isogenes in vivo, for in vivo screening and
CC testing of drugs targeted to GRM8, and for testing the efficacy of
CC therapeutic agents and compounds for treating GRM8-associated conditions
CC in a biological system. Sequences ABQ72863-ABQ72904 represent sequences
CC that are specifically claimed as components of primers used to detect
CC polymorphisms in the GRM8 gene by primer extension
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGGCAGAAG 20
|||.||||||
Db 1 TGGTCAGAAG 10

RESULT 92
ABK96537
ID ABK96537 standard; DNA; 10 BP.
XX
AC ABK96537;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human PLAU gene, primer extension primer 3' terminus #10.
XX
KW Human; ss; primer; Plasminogen activator; urokinase; PLAU; cancer;
KW cytostatic; serine protease; thrombolytic disorder; isogene; PCR;
KW pulmonary embolism; chromosome 10q24-qter; haplotype; genotype; SNP;
KW single nucleotide polymorphism; thrombolytic; gene therapy;
KW primer extension.
XX
OS Homo sapiens.
XX
PN WO200240503-A2.
XX
PD 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-US044001.
XX
PR 17-NOV-2000; 2000US-0249703P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Bentivegna SC, Koshy B;
XX
DR WPI; 2002-519370/55.
XX
PT Genetic variants of Plasminogen activator, Urokinase (PLAU) isogenes,
PT useful for improving efficiency and reliability in drug development for
PT treating thrombolytic disorders and cancer.
XX
PS Claim 16; Page 14; 92pp; English.
XX
CC The invention relates to a polynucleotide comprising a first nucleotide
CC sequence (NS1) comprising a PLAU (plasminogen activator, urokinase, a
CC serine protease) isogene selected from isogenes 1-9 and 11-20 given in
CC the specification, where each isogene comprises the regions of the PLAU
CC gene or cDNA and is further defined by the corresponding sequence of
CC polymorphisms (defining single nucleotide polymorphisms, SNP). Also
CC included are methods of haplotyping/genotyping (and predicting the
CC haplotype/genotype of the PLAU gene of an individual, identifying an
CC association between a trait and at least one haplotype or haplotype pair
CC of the PLAU gene, an isolated oligonucleotide for detecting a
CC polymorphism in the PLAU gene, a recombinant non-human organism
CC transformed or transfected with the gene or cDNA, fragments of the
CC polynucleotides of at least 10 base pairs encompassing a polymorphic
CC site, an isolated polymorphic variant PLAU protein or fragment, an
CC isolated monoclonal antibody specific for PLAU, a computer system for
CC storing and analysing polymorphism data for the PLAU gene and a genome
CC anthology for the PLAU gene. PLAU is useful in screening for drugs
CC targeting PLAU that are useful for treating thrombolytic disorders and
CC cancers. The methods are useful for improving the efficiency and
CC reliability of the discovery and development of drugs for treating
CC diseases associated with PLAU activity, in validating PLAU as a drug
CC target and in the design of clinical trials for treating a specific
CC condition of disease associated with PLAU activity. The antibody is
CC useful in diagnostic, prognostic and therapeutic methods. PLAU
CC polynucleotides are useful in studying the expression and function of
CC PLAU, and in expressing PLAU protein for use in screening for candidate
CC drugs to treat diseases related to PLAU activity. The gene for PLAU is
CC located on chromosome 10q24-qter. The present sequence is the 3' terminus
CC of an allele specific primer used to amplify PLAU polynucleotides with a
CC specific polymorphism using the technique of primer extension
XX
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;

```
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              | ||||||||
Db          1 TCCTTGGGCA 10


RESULT 93
ACF04526/c
ID   ACF04526 standard; DNA; 10 BP.
XX
AC   ACF04526;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Stuffer sequence used in NA detection by mass spectrometry #9.
XX
KW   Mass spectrometry; nucleic acid sequence detection; stuffer sequence; ds.
XX
OS   Synthetic.
XX
PN   WO2003060163-A2.
XX
PD   24-JUL-2003.
XX
PF   30-DEC-2002; 2002WO-NL000872.
XX
PR   28-DEC-2001; 2001EP-00205114.
XX
PA   (KEYG-) KEYGENE NV.
XX
PI   Van Eijk MJT,  Van Schaik C;
XX
DR   WPI; 2003-598543/56.
XX
PT   Determining the presence or absence of target sequences in nucleic acid
PT   samples, useful for e.g. genetic mapping or DNA fingerprinting, comprises
PT   employing an oligonucleotide ligation assay in combination with mass
PT   spectrometry.
XX
PS   Example 3; Page 27; 68pp; English.
XX
CC   The present invention relates to a method of determining the presence or
CC   absence of at least one target sequence in a nucleic acid sample, which
CC   comprises employing an oligonucleotide ligation assay in combination with
CC   a detection method based upon molecular mass, preferably mass
CC   spectrometry. The method is useful for high-throughput detection of a
CC   multiplicity of target nucleotide sequences, for detecting polymorphisms
CC   (preferably single nucleotide polymorphism), for transcript profiling,
CC   for detecting quantitative abundance of target nucleic acid sequences,
CC   for genetic mapping, gene discovery, marker-assisted selection, seed
CC   quality control, hybrid selection, QTL mapping, bulked segregant
CC   analysis, DNA fingerprinting and for disclosing information relating to
CC   traits, disease resistance, yield, hybrid vigor, and/or gene function.
CC   The set of oligonucleotide probes, which comprises a probe for each
CC   allele of a single nucleotide polymorphism, is useful for determining the
CC   presence or absence of at least one target sequence in a nucleic acid
CC   sample. The present sequence is a stuffer sequence used in the
CC   exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              |||||| |||
Db         10 CCCACCCTCT 1


RESULT 94
AAA16595/c
ID   AAA16595 standard; DNA; 11 BP.
XX
AC   AAA16595;
XX
DT   16-JUN-2000  (first entry)
XX
DE   Human MN gene 5' donor consensus splice sequence SEQ ID NO:73.
XX
KW   Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW   oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW   MN/CA IX isoenzyme; ds.
XX
OS   Homo sapiens.
XX
PN   US6027887-A.
XX
PD   22-FEB-2000.
XX
PF   24-JAN-1997;   97US-00787739.
XX
PR   21-OCT-1992;   92US-00964589.
PR   30-DEC-1993;   93US-00177093.
PR   15-JUN-1994;   94US-00260190.
PR   07-JUN-1995;   95US-00477504.
PR   07-JUN-1995;   95US-00481658.
PR   07-JUN-1995;   95US-00485049.
PR   07-JUN-1995;   95US-00485862.
PR   07-JUN-1995;   95US-00485863.
PR   07-JUN-1995;   95US-00486756.
PR   07-JUN-1995;   95US-00487077.
XX
PA   (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX
PI   Pastorek J,  Zavada J,  Pastorekova S;
XX
DR   WPI; 2000-194827/17.
XX
PT   Nucleic acid based assay for diagnosing a wide variety of
PT   preneoplastic/neoplastic disease comprises screening for the presence of
PT   abnormal MN gene expression in a vertebrate.
XX
PS   Disclosure; Col 16; 87pp; English.
XX
CC   The present invention describes a method of screening for
CC   preneoplastic/neoplastic disease. The method comprises: (1) determining
CC   whether abnormal MN gene expression is present in a vertebrate; and (2)
CC   if abnormal MN gene expression is determined to be present in the
CC   vertebrate, determining that the vertebrate has a significant risk of
CC   having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC   encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC   protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC   is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC   in a vertebrate, preferably a human. The disease detected is mammary,
CC   bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC   vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC   testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC   duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC   mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC   mucosa, pancreatic duct epithelium or liver duct epithelium
CC   preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to
CC   AAY53245 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1
```

```
RESULT 95
AAA52514/c
ID   AAA52514 standard; DNA; 11 BP.
XX
AC   AAA52514;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Human MN gene intron 7 splice donor sequence.
XX
KW   MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW   proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW   abnormal expression; neoplastic disease; cancer; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200024913-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-US024879.
XX
PR   23-OCT-1998;   98US-00177776.
PR   23-OCT-1998;   98US-00178115.
XX
PA   (FARB ) BAYER CORP.
PA   (VIRO-) INST VIROLOGY.
XX
PI   Zavada J,  Pastorekova S,  Pastorek J;
XX
DR   WPI; 2000-350752/30.
XX
PT   A molecule which specifically binds to a site on MN protein (oncoprotein)
PT   and prevents adhesion of vertebrate cells to the protein, useful for
PT   treating preneoplastic or neoplastic diseases such as cancer.
XX
PS   Disclosure; Page 26; 154pp; English.
XX
CC   The invention relates to the inhibition of cell adhesion mediated by the
CC   MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC   protein). The MN protein is a tumour-associated adhesion molecule which
CC   comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC   protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC   Abnormal expression of the MN protein is associated with tumorigenicity.
CC   The invention encompasses molecules (e.g., proteins and peptides) which
CC   which specifically bind to a site on the MN protein, thereby preventing
CC   adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC   also encompasses MN proteins or MN protein fragments which can be added
CC   to the extracellular environment to prevent the adhesion of vertebrate
CC   cells to each other. The invention also relates to the identification of
CC   the binding site of the MN protein and to a method of identifying a site
CC   on an MN protein to which cells adhere, comprising testing a series of
CC   overlapping peptides from the protein in a cell adhesion assay. The
CC   invention encompasses a vector comprising an expression control sequence
CC   operatively linked to a nucleic acid encoding the variable domains of a
CC   MN-specific antibody, where the domains are separated by a flexible
CC   linker peptide (AAB03035) and the vector inhibits the growth of a
CC   vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC   protein. The invention also encompasses a vector comprising a nucleic
CC   acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC   gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC   neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC   gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins
CC   and peptides, and expression vectors encoding such proteins and peptides
CC   are useful for treating patients with preneoplastic or neoplastic disease
CC   (e.g., cancers) associated with or characterised by abnormal MN
CC   expression. The present sequence represents a fragment of the human MN
CC   gene (AAA52462) specified in the invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||||| ||
Db         10 CCCACCTGCT 1


RESULT 96
ABQ87504
ID   ABQ87504 standard; cDNA; 11 BP.
XX
AC   ABQ87504;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 1259.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 89; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              |||||| |||
Db          2 CACCTTATTG 11


RESULT 97
ABQ87500
ID   ABQ87500 standard; cDNA; 11 BP.
XX
AC   ABQ87500;
XX
DT   10-SEP-2002  (first entry)
```

XX
DE Human skin stress/ageing related EST SEQ ID NO 1255.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 89; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CACCTTCTTG 12
||||||||.|
Db 2 CACCTTCTGG 11

RESULT 98
ABQ86415/c
ID ABQ86415 standard; cDNA; 11 BP.
XX
AC ABQ86415;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 170.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 44; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCACCTTCTT 11
|||| |||||
Db 11 CCACTTTCTT 2

RESULT 99
ABV66344/c
ID ABV66344 standard; cDNA; 11 BP.
XX
AC ABV66344;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4130.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 139; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)

```
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 5 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGGCA 16
              || |||||||
Db         11 TTTTTGGGCA 2


RESULT 100
ABV62764/c
ID   ABV62764 standard; cDNA; 11 BP.
XX
AC   ABV62764;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 550.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 40; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||||| |||
Db         10 CCACCTCCTT 1


RESULT 101
ABV70185/c
ID   ABV70185 standard; cDNA; 11 BP.
XX
AC   ABV70185;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7971.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 254; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||||| |||
Db         10 CCACCTCCTT 1


RESULT 102
ABV62651
ID   ABV62651 standard; cDNA; 11 BP.
XX
AC   ABV62651;
```

```
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 437.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 37; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 0 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||| ||||||
Db          2 CCCGCCTTCT 11


RESULT 103
ABV67006/c
ID   ABV67006 standard; cDNA; 11 BP.
XX
AC   ABV67006;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4792.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 157; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CCACCTTCTT 11
              |||| |||||
Db         11 CCACTTTCTT 2


RESULT 104
ABV67047
ID   ABV67047 standard; cDNA; 11 BP.
XX
AC   ABV67047;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4833.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
```

PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 158; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CACCTTCTTG 12
||||||||| |
Db 2 CACCTTCTGG 11

RESULT 105
ABV64836/c
ID ABV64836 standard; cDNA; 11 BP.
XX
AC ABV64836;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2622.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 98; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCACCTTCTT 11
||||||| ||
Db 10 CCACCTTTTT 1

RESULT 106
ABV67092
ID ABV67092 standard; cDNA; 11 BP.
XX
AC ABV67092;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4878.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 159; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCACCTTCTT 11
|||||| |||

```
Db          1 CCACCTGCTT 10


RESULT 107
ABV67518
ID   ABV67518 standard; cDNA; 11 BP.
XX
AC   ABV67518;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5304.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 171; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              ||||| ||||
Db          2 TTGGGTAGAA 11


RESULT 108
ABV72108
ID   ABV72108 standard; cDNA; 11 BP.
XX
AC   ABV72108;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9894.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 323; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CTTGGGCAGA 18
              ||||||| |
Db          2 CTTGGGCACA 11


RESULT 109
ABV62632/c
ID   ABV62632 standard; cDNA; 11 BP.
XX
AC   ABV62632;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 418.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
```

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XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 37; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              ||| ||||||
Db         11 CACTTTCTTG 2


RESULT 110
ABV65381/c
ID   ABV65381 standard; cDNA; 11 BP.
XX
AC   ABV65381;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3167.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 113; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              |||||| |||
Db         10 CCCACCCTCT 1


RESULT 111
ABV67446
ID   ABV67446 standard; cDNA; 11 BP.
XX
AC   ABV67446;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5232.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 169; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
```

```
SQ   Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              |||||| |||
Db          2 CACCTTATTG 11


RESULT 112
ABV66204
ID   ABV66204 standard; cDNA; 11 BP.
XX
AC   ABV66204;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3990.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 135; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 TTGGGCAGAA 19
              |||||||| |
Db          1 TTGGGCAGGA 10


RESULT 113
ABV65314
ID   ABV65314 standard; cDNA; 11 BP.
XX
AC   ABV65314;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3100.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 111; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCCACCTTCT 10
              ||||| ||||
Db          2 CCCACTTTCT 11


RESULT 114
ABV70072
ID   ABV70072 standard; cDNA; 11 BP.
XX
AC   ABV70072;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7858.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
```

XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 250; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCACCTTCT 10
||| ||||||
Db 2 CCCGCCTTCT 11

RESULT 115
ABV69202/c
ID ABV69202 standard; cDNA; 11 BP.
XX
AC ABV69202;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6988.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 219; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 6 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTTCTTGGGC 15
||||||| ||
Db 10 CTTCTTGTGC 1

RESULT 116
ABV70053/c
ID ABV70053 standard; cDNA; 11 BP.
XX
AC ABV70053;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7839.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 250; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to

```
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CACCTTCTTG 12
              ||| ||||||
Db         11 CACTTTCTTG 2


RESULT 117
AAT09397/c
ID   AAT09397 standard; DNA; 8 BP.
XX
AC   AAT09397;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 4 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTG 12
              ||||||||
Db          8 CCTTCTTG 1


RESULT 118
AAT09546
ID   AAT09546 standard; DNA; 8 BP.
XX
AC   AAT09546;
XX
DT   25-MAR-2003  (revised)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 0 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTG 12
              ||||||||
Db          1 CCTTCTTG 8


RESULT 119
AAT09415/c
ID   AAT09415 standard; DNA; 8 BP.
XX
AC   AAT09415;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1996  (first entry)
XX
```

DE 5'-primer used for characterisation of human biological samples.
XX
KW 5'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US006032.
XX
PR 16-MAY-1994; 94US-00242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX
PS Claim 5; Page 44; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer kit
CC with 1361 possible primer pairs. The kit is used in a new method for the
CC characterisation of nucleic acid sequences obtd. from human biological
CC samples, which comprises PCR amplification and indexing of the prods.
CC w.r.t the primer pair that hybridised to its delineating subsequences.
CC The method may be used in the identification, cloning and analysis of
CC genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 8 BP; 4 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTTCTTGG 13
||||||||
Db 8 CTTCTTGG 1

RESULT 120
AAT09568
ID AAT09568 standard; DNA; 8 BP.
XX
AC AAT09568;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1996 (first entry)
XX
DE 3'-primer used for characterisation of human biological samples.
XX
KW 3'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US006032.
XX
PR 16-MAY-1994; 94US-00242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX
PS Disclosure; Page 19; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer kit
CC with 1361 possible primer pairs. The kit is used in a new method for the
CC characterisation of nucleic acid sequences obtd. from human biological
CC samples, which comprises PCR amplification and indexing of the prods.
CC w.r.t the primer pair that hybridised to its delineating subsequences.
CC The method may be used in the identification, cloning and analysis of
CC genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 8 BP; 0 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTTCTTGG 13
||||||||
Db 1 CTTCTTGG 8

RESULT 121
ABQ71965/c
ID ABQ71965 standard; DNA; 9 BP.
XX
AC ABQ71965;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2263.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 59; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CACCTTCT 10
||||||||
Db 9 CACCTTCT 2

RESULT 122
ABQ71964/c
ID ABQ71964 standard; DNA; 9 BP.
XX
AC ABQ71964;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2262.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 59; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CACCTTCT 10
||||||||
Db 9 CACCTTCT 2

RESULT 123
ABQ71781/c
ID ABQ71781 standard; DNA; 9 BP.
XX
AC ABQ71781;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2079.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 55; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to

CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACCTT 8
||||||||
Db 8 CCCACCTT 1

RESULT 124
ABQ71780/c
ID ABQ71780 standard; DNA; 9 BP.
XX
AC ABQ71780;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2078.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 55; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACCTT 8
||||||||
Db 8 CCCACCTT 1

RESULT 125
ACD06034
ID ACD06034 standard; DNA; 9 BP.
XX
AC ACD06034;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human VEGF-targeted zinc finger protein target sequence #7.
XX
KW Zinc finger protein; antiarteriosclerotic; vasotropic; antiarthritic;
KW cytostatic; antipsoriatic; ophthalmological; antidiabetic; antiulcer;
KW vulnerary; gene therapy; vascular endothelial growth factor; VEGF;
KW angiogenesis; atherosclerosis; ischaemia; arthritis; tumour; psoriasis;
KW diabetic retinopathy; ulcer; wound; ds.
XX
OS Homo sapiens.
XX
PN US2003044404-A1.
XX
PD 06-MAR-2003.
XX
PF 30-APR-2001; 2001US-00846033.
XX
PR 07-DEC-2000; 2000US-00733604.
PR 12-DEC-2000; 2000US-00736083.
XX
PA (REBA/) REBAR E.
PA (JAMI/) JAMIESON A.
PA (LIUQ/) LIU Q.
PA (LIUP/) LIU P.
PA (WOLF/) WOLFFE A.
PA (EISE/) EISENBERG S P.
PA (JARV/) JARVIS E.
XX
PI Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;
PI Jarvis E;
XX
DR WPI; 2003-456550/43.
XX
PT New zinc finger protein that binds to a target site in the human vascular
PT endothelial growth factor gene, useful for regulating angiogenesis, e.g.
PT in the treatment of atherosclerosis, ischemia, arthritis, tumors, ulcer
PT or wounds.
XX
PS Example 6; Page 42; 75pp; English.
XX
CC The invention describes a zinc finger protein (ZFP) that binds to a
CC target site having a nucleotide sequence of any of the human vascular
CC endothelial growth factor (VEGF) genes listed in the specification. The
CC composition and methods are useful in regulating angiogenesis, such as in
CC the treatment of atherosclerosis, ischaemia, arthritis, tumours,
CC psoriasis, diabetic retinopathy, ulcer or wounds. The composition may

```
CC   also be used in screening for agents capable of modulating angiogenesis,
CC   and in various diagnostic applications. This sequence represents a
CC   vascular endothelial growth factor (VEGF) targeting zinc finger protein
CC   zinc finger domain target DNA
XX
SQ   Sequence 9 BP; 2 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGCAGA 18
              ||||||||
Db          1 TGGGCAGA 8


RESULT 126
ACD19256
ID   ACD19256 standard; DNA; 9 BP.
XX
AC   ACD19256;
XX
DT   22-AUG-2003  (first entry)
XX
DE   Human VEGF-targeted ZFP HUM 19A target sequence.
XX
KW   Zinc finger protein; vascular endothelial growth factor; VEGF; ischaemia;
KW   atherosclerosis; tumour; arthritis; bone injury; wound; ulcer; surgery;
KW   angiogenesis; pregnancy; embryogenesis; ds; human.
XX
OS   Homo sapiens.
XX
PN   US2003021776-A1.
XX
PD   30-JAN-2003.
XX
PF   06-DEC-2001; 2001US-00006069.
XX
PR   07-DEC-2000; 2000US-00733604.
PR   12-DEC-2000; 2000US-00736083.
PR   30-APR-2001; 2001US-00846033.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Rebar E,  Jamieson A,  Liu Q,  Liu P,  Wolffe A,  Eisenberg SP;
PI   Jarvis E;
XX
DR   WPI; 2003-466074/44.
XX
PT   Novel zinc finger protein that binds to a target site, useful for
PT   modulating vascular endothelial growth factor gene expression, for
PT   modulating angiogenesis, for wound healing and for treating ischemia.
XX
PS   Disclosure; Page 43; 120pp; English.
XX
CC   The invention relates to a zinc finger protein that binds to a target
CC   site. The zinc finger protein is useful for modulating expression of a
CC   vascular endothelial growth factor (VEGF) gene. The expression of a
CC   number of splice variants of VEGF gene is modulated. A number of target
CC   sites are contacted with a number of zinc finger proteins and each zinc
CC   finger protein binds to a distinct target site. The zinc finger protein
CC   is administered in combination with a delivery vehicle, or its nucleic
CC   acid is administered into the cell, either in naked form or delivered in
CC   an expression vector. The zinc finger protein or nucleic acid is useful
CC   for treating a disease or injury such as atherosclerosis, ischaemia,
CC   tumour, arthritis, bone injury, wounds and ulcer in a subject. The zinc
CC   finger protein is also useful for modulating angiogenesis, by introducing
CC   the zinc finger protein into an animal, where the animal has a genome
CC   comprising a target site within a VEGF gene. The zinc finger protein is
CC   also useful for screening for a modulator of expression of a VEGF gene.
CC   The zinc finger protein and nucleic acid are also useful to promote
CC   development of the corpus luteum and endometrium, which is useful for
CC   initiating and/or maintaining pregnancy and for supporting embryogenesis.
CC   The zinc finger protein and its nucleic acid are also useful in surgical
CC   applications. The present sequence represents a human VEGF targetted zinc
CC   finger protein ZFP target sequence
XX
SQ   Sequence 9 BP; 2 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGGCAGA 18
              ||||||||
Db          1 TGGGCAGA 8


RESULT 127
ADA64108/c
ID   ADA64108 standard; DNA; 9 BP.
XX
AC   ADA64108;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #566.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 22; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          8 CCCACCTT 1
```

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RESULT 128
ADA64291/c
ID   ADA64291 standard; DNA; 9 BP.
XX
AC   ADA64291;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #749.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db          9 CACCTTCT 2


RESULT 129
ADA64292/c
ID   ADA64292 standard; DNA; 9 BP.
XX
AC   ADA64292;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #750.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db          9 CACCTTCT 2


RESULT 130
ADA64107/c
ID   ADA64107 standard; DNA; 9 BP.
XX
AC   ADA64107;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #565.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
```

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XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 22; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          8 CCCACCTT 1


RESULT 131
AAZ79378/c
ID   AAZ79378 standard; DNA; 10 BP.
XX
AC   AAZ79378;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1806.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 116; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
              ||||||||
Db          9 GGCAGAAG 2


RESULT 132
AAZ77868
ID   AAZ77868 standard; DNA; 10 BP.
XX
AC   AAZ77868;
XX
DT   10-APR-2000  (first entry)
XX
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DE   Human dendritic cell SAGE tag, SEQ ID NO:296.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 72; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
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CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
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CC   complex) and subsequent recognition by T-cell receptors is alone
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CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
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CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
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CC   expression of these genes. Detection of the dendritic cell differentially
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CC   them are used in gene therapy. Co-administration of tumour antigens and
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CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db          2 CACCTTCT 9


RESULT 133
AAZ78273/c
ID   AAZ78273 standard; DNA; 10 BP.
XX
AC   AAZ78273;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:701.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
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PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 85; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
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CC   (APC)-associated costimulatory factors play an important role in the
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CC   the tumour cells, immunostimulatory cofactors also being required for
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CC   They may be used in vaccines to induce an immune response, particularly
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CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GGCAGAAG 20
               ||||||||
Db           9 GGCAGAAG 2


RESULT 134
AAZ78942
ID   AAZ78942 standard; DNA; 10 BP.
XX
AC   AAZ78942;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1370.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
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PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 104; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
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CC   the tumour cells, immunostimulatory cofactors also being required for
```

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CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
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CC   secretion of T cell growth factors and secretion of chemokines for
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XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
              ||||||||
Db          1 GGCAGAAG 8


RESULT 135
AAZ77770
ID   AAZ77770 standard; DNA; 10 BP.
XX
AC   AAZ77770;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:198.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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OS   Homo sapiens.
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PN   WO9965924-A2.
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PD   23-DEC-1999.
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PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
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PR   19-JUN-1998;   98US-0090042P.
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PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
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PI   Roberts BL,  Shankara S;
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DR   WPI; 2000-106077/09.
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XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAA 19
              ||||||||
Db          1 GGGCAGAA 8


RESULT 136
AAZ77870
ID   AAZ77870 standard; DNA; 10 BP.
XX
AC   AAZ77870;
XX
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DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:298.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
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XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
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PR 19-JUN-1998; 98US-0090041P.
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PR 19-JUN-1998; 98US-0090043P.
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PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
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XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
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DR WPI; 2000-106077/09.
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CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACCTT 8
||||||||
Db 3 CCCACCTT 10

RESULT 137
AAZ79364
ID AAZ79364 standard; DNA; 10 BP.
XX
AC AAZ79364;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1792.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.

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PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 116; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTG 12
              ||||||||
Db          1 CCTTCTTG 8


RESULT 138
AAZ79551/c
ID   AAZ79551 standard; DNA; 10 BP.
XX
AC   AAZ79551;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1979.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 121; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
```

```
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db          9 CCACCTTC 2


RESULT 139
AAZ83134
ID   AAZ83134 standard; DNA; 10 BP.
XX
AC   AAZ83134;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2368.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 123; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
              ||||||||
Db          3 GGCAGAAG 10


RESULT 140
AAZ81919
ID   AAZ81919 standard; DNA; 10 BP.
XX
AC   AAZ81919;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1153.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
```

```
XX
PS   Claim 1; Page 89; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGG 14
              ||||||||
Db          1 TTCTTGGG 8


RESULT 141
AAZ84193/c
ID   AAZ84193 standard; DNA; 10 BP.
XX
AC   AAZ84193;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3427.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 150; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db         10 CCCACCTT 3


RESULT 142
AAZ82122/c
ID   AAZ82122 standard; DNA; 10 BP.
XX
AC   AAZ82122;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1356.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
```

```
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 95; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GGCAGAAG 20
               ||||||||
Db          10 GGCAGAAG 3


RESULT 143
AAZ83647
ID   AAZ83647 standard; DNA; 10 BP.
XX
AC   AAZ83647;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2881.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 136; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           3 CACCTTCT 10
               ||||||||
Db           2 CACCTTCT 9


RESULT 144
AAZ83418
ID   AAZ83418 standard; DNA; 10 BP.
XX
AC   AAZ83418;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2652.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
```

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XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 130; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAA 19
              ||||||||
Db          2 GGGCAGAA 9


RESULT 145
AAZ82784/c
ID   AAZ82784 standard; DNA; 10 BP.
XX
AC   AAZ82784;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2018.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 113; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db         10 CCACCTTC 3


RESULT 146
AAZ85883
ID   AAZ85883 standard; DNA; 10 BP.
XX
AC   AAZ85883;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5117.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
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XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 194; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db          3 CCACCTTC 10


RESULT 147
AAZ86535/c
ID   AAZ86535 standard; DNA; 10 BP.
XX
AC   AAZ86535;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5769.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 210; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db          9 CCACCTTC 2


RESULT 148
AAZ81064/c
ID   AAZ81064 standard; DNA; 10 BP.
XX
AC   AAZ81064;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #298.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
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PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 66; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCACCTTC 9
||||||||
Db 9 CCACCTTC 2

RESULT 149
AAZ83296/c
ID AAZ83296 standard; DNA; 10 BP.
XX
AC AAZ83296;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2530.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.

XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 127; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GGCAGAAG 20
||||||||
Db 9 GGCAGAAG 2

RESULT 150
AAZ84897/c
ID AAZ84897 standard; DNA; 10 BP.
XX
AC AAZ84897;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4131.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.

XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 169; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CACCTTCT 10
||||||||
Db 10 CACCTTCT 3

RESULT 151
AAZ81128
ID AAZ81128 standard; DNA; 10 BP.
XX
AC AAZ81128;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #362.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.

XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 67; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGGCAGAA 19
||||||||
Db 1 GGGCAGAA 8

RESULT 152
AAZ83682/c
ID AAZ83682 standard; DNA; 10 BP.
XX
AC AAZ83682;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2916.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.

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XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 137; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db          8 CCACCTTC 1


RESULT 153
AAZ83851/c
ID   AAZ83851 standard; DNA; 10 BP.
XX
AC   AAZ83851;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3085.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 141; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAA 19
              ||||||||
Db          8 GGGCAGAA 1


RESULT 154
AAZ79914
ID   AAZ79914 standard; DNA; 10 BP.
XX
AC   AAZ79914;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell preferentially expressed SAGE tag, SEQ ID NO:205.
XX
KW   SAGE tag; serial analysis of gene expression; diagnosis;
```

```
KW   differential gene expression; characterisation; targetted expression;
KW   tumour; cancer; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966303-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-US013820.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106132/09.
XX
PT   New polynucleotide useful in cancer immunotherapy.
XX
PS   Claim 1; Page 63; 97pp; English.
XX
CC   Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts which are
CC   differentially expressed in a variety of normal or malignant cell types.
CC   Some of the transcripts correspond to known genes or ESTs (expressed
CC   sequence tags) which were previously unknown to be preferentially or
CC   differentially expressed in that particular cell type, while other
CC   transcripts correspond to novel genes. The invention also provides a
CC   nucleotide comprising a promoter sequence derived from one of the
CC   differentially expressed genes, which may optionally be operably linked
CC   to a foreign nucleotide sequence, and gene delivery vehicles and host
CC   cells comprising the polynucleotides of the invention. A nucleotide
CC   comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures
CC   to characterise a cell of a specific tissue type and to determine whether
CC   it is normal or malignant. They may be used to screen for agents that
CC   modulate expression of differentially expressed genes compound. The
CC   promoter/foreign gene construct of the invention may be used for
CC   targetted expression of the foreign gene in a particular cell type. For
CC   example, a promoter derived from a gene preferentially expressed in
CC   dendritic cells (antigen-presenting cells, or APCs), may be operably
CC   linked to a sequence encoding an immunostimulatory molecule and a
CC   sequence encoding an antigen. Such a construct could be transduced into
CC   APCs and would be useful for inducing an immune response by educating
CC   immune effector cells in vivo, or in cancer immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACCTT 8
              ||||||||
Db          3 CCCACCTT 10


RESULT 155
AAH64317/c
ID   AAH64317 standard; cDNA; 10 BP.
XX
AC   AAH64317;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1157.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 65; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CACCTTCT 10
              ||||||||
Db         10 CACCTTCT 3


RESULT 156
AAH63292
ID   AAH63292 standard; cDNA; 10 BP.
```

XX
AC AAH63292;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 132.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 11; Page 42; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTTCTTG 12
||||||||
Db 1 CCTTCTTG 8

RESULT 157
AAF69638/c
ID AAF69638 standard; DNA; 10 BP.
XX
AC AAF69638;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene probe #278.
XX
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200104270-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019094.
XX
PR 13-JUL-1999; 99US-0143435P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
DR WPI; 2001-103078/11.
XX
PT New isolated polynucleotide useful for the identification of therapeutics
PT in allergic diseases is new.
XX
PS Disclosure; Page 46; 188pp; English.
XX
CC The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha
CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a probe for human IL4R-alpha
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCACCTTC 9
||||||||
Db 10 CCACCTTC 3

RESULT 158
AAF35751/c
ID AAF35751 standard; DNA; 10 BP.
XX
AC AAF35751;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2490.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX

PS Example; Page 88; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCTTCTT 11
||||||||
Db 8 ACCTTCTT 1

RESULT 159
AAF39472
ID AAF39472 standard; DNA; 10 BP.
XX
AC AAF39472;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6211.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 221; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTTCTTGG 13
||||||||
Db 2 CTTCTTGG 9

RESULT 160
AAF39102
ID AAF39102 standard; DNA; 10 BP.
XX
AC AAF39102;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5841.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX

DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 208; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTGGGCAG 17
||||||||
Db 3 TTGGGCAG 10

RESULT 161
AAF41579
ID AAF41579 standard; DNA; 10 BP.
XX
AC AAF41579;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8318.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 297; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTTCTTGG 13
||||||||
Db 1 CTTCTTGG 8

RESULT 162
AAF43940/c
ID AAF43940 standard; DNA; 10 BP.
XX
AC AAF43940;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12079.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX

```
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 381; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGGCAGAA 19
              ||||||||
Db          9 GGGCAGAA 2


RESULT 163
AAF34735/c
ID   AAF34735 standard; DNA; 10 BP.
XX
AC   AAF34735;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1474.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 52; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCTTCTTG 12
              ||||||||
Db          9 CCTTCTTG 2


RESULT 164
AAF34229/c
ID   AAF34229 standard; DNA; 10 BP.
XX
AC   AAF34229;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:968.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
```

PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 34; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CACCTTCT 10
||||||||
Db 10 CACCTTCT 3

RESULT 165
AAF37328/c
ID AAF37328 standard; DNA; 10 BP.
XX
AC AAF37328;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4067.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 145; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTTCTTG 12
||||||||
Db 8 CCTTCTTG 1

RESULT 166
ABK24258/c
ID ABK24258 standard; DNA; 10 BP.
XX
AC ABK24258;
XX
DT 09-APR-2002 (first entry)
XX
DE Retinaldehyde-binding protein 1 ASO primer extension primer #31.
XX
KW Human; retinaldehyde-binding protein 1; ss; RLBP1; haplotype; primer;

```
KW   genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR;
KW   chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.
XX
OS   Homo sapiens.
XX
PN   WO200192278-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US017252.
XX
PR   26-MAY-2000; 2000US-0207618P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-122053/16.
XX
PT   New genetic variants having polymorphisms in the retinaldehyde-binding
PT   protein 1 gene, useful for studying the function of and for expressing
PT   RLBP1 protein for use in screening drugs for treating diseases related to
PT   RLBP1 activity.
XX
PS   Claim 18; Page 14; 107pp; English.
XX
CC   The invention relates to an isolated polynucleotide, which comprises
CC   genes and haplotypes of the retinaldehyde-binding protein 1 (RLBP1) gene.
CC   The polynucleotide comprises polymorphic sites in the RLBP1 gene, which
CC   are referred to as PS1-24 to designate the order in which they are
CC   located in the gene. Also included are methods for haplotyping or
CC   genotyping the RLBP1 gene of an individual, a method for predicting a
CC   haplotype pair for the RLBP1 gene of an individual, a method for
CC   identifying an association between a trait and at least one haplotype or
CC   haplotype pair of the RLBP1 gene, a composition comprising at least one
CC   genotyping oligonucleotide for detecting a polymorphism in the RLBP1 gene
CC   at a PS consisting of PS1-PS24, a kit for genotyping the RLBP1 gene of an
CC   individual comprising a set of oligonucleotides designed to genotype each
CC   of PS1-PS24 recombinant non-human organisms transformed or transfected
CC   with the isolated polynucleotide, where the organism expresses a RLBP1
CC   protein encoded by the first nucleotide sequence or expresses an RLBP1
CC   protein encoded by the polymorphic variant sequence, an isolated
CC   polypeptide comprising an amino acid sequence that is a polymorphic
CC   variant of a reference sequence for the RLBP1 protein or its fragment, an
CC   anti-RLBP1 antibody, a method for screening for drugs targeting the
CC   isolated polypeptide, and a computer system for storing and analysing
CC   polymorphism data for the RLBP1 oncogene gene. The polynucleotide
CC   comprising polymorphisms in the RLBP1 gene is useful in studying the
CC   expression and function of RLBP1, and in expressing RLBP1 protein for use
CC   in screening candidate drugs to treat diseases related to RLBP1 activity
CC   (e.g autosomal recessive retinitis pigmentosa (arRP). The methods and
CC   haplotypes are useful in improving the efficiency and output of several
CC   steps in the drug discovery and development process, including target
CC   validation, identifying lead compounds, and early phase clinical trials.
CC   These are also useful for designing clinical trials of candidate drugs
CC   for treating a specific condition or disease, as well as for screening
CC   compounds targeting RLBP1 to treat a specific condition or disease
CC   predicted to be associated with RLBP1 activity. The kit and method are
CC   useful for determining whether an individual has one of the haplotypes or
CC   haplotype pairs cited above. The transgenic animals are useful for
CC   studying expression of the RLBP1 isogenes in vivo, for in vivo screening
CC   and testing of drugs targeted against RLBP1 protein, and for testing the
CC   efficacy of therapeutic agents and compounds for retinal diseases in a
CC   biological system. The gene for RLBP1 is located on chromosome 15q26. The
CC   present sequence is an allele specific oligonucleotide (ASO) PCR primer
CC   for amplifying a nucleic acid containing a polymorphic RLBP sequence,
CC   using the primer extension method
XX
SQ   Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TCTTGGGC 15
              ||||||||
Db          8 TCTTGGGC 1


RESULT 167
ABK23697/c
ID   ABK23697 standard; DNA; 10 BP.
XX
AC   ABK23697;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #286 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
              ||||||||
Db          9 GGCAGAAG 2


RESULT 168
AAS16818
ID   AAS16818 standard; DNA; 10 BP.
XX
AC   AAS16818;
XX
DT   14-FEB-2002  (first entry)
XX
```

DE Human apolipoprotein C1 (APOC1) gene PCR primer #4.
XX
KW Human; apolipoprotein C1; APOC1; single nucleotide polymorphism;
KW haplotyping; haplotype pair; hypercholesterolaemia; nootropic; SDAT; ss;
KW senile dementia of Alzheimer's type; neuroprotective; antilipaemic;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200177129-A2.
XX
PD 18-OCT-2001.
XX
PF 10-APR-2001; 2001WO-US011808.
XX
PR 11-APR-2000; 2000US-0196545P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
XX
DR WPI; 2002-041286/05.
XX
PT New haplotypes of the human apolipoprotein C1 gene, useful to detect and
PT find treatment for disease associated with its activity such as
PT hypercholestrolemia and Alzheimer's disease.
XX
PS Claim 18; Page 13; 51pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the human
CC apolipoprotein C1 (APOC1) gene. Haplotyping the APOC1 gene of an
CC individual, comprises determining if the individual has one of the APOC1
CC haplotypes or haplotype pairs fully defined in the specification.
CC Genotyping the APOC1 gene of an individual, comprises determining the
CC identity of the nucleotide pair at one or more polymorphic sites and
CC predicting a haplotype pair for the APOC1 gene of an individual by
CC enumerating all possible haplotype pairs which are consistent with the
CC genotype, comparing the possible haplotype pairs to the data detailed in
CC the specification and assigning a haplotype pair to the individual that
CC is consistent with the data. Identifying an association between a trait
CC and a haplotype or haplotype pair of the APOC1 gene, comprises comparing
CC the frequency of the haplotype/haplotype pair in a population exhibiting
CC the trait with that of a reference population, where the
CC haplotype/haplotype pair is one described in the specification and a
CC higher frequency in the trait population indicates the trait is
CC associated with the haplotype. The sequences and methods of the invention
CC are used to diagnose and develop treatment for disease associated with
CC APOC1 activity, such as hypercholesterolaemia and senile dementia of
CC Alzheimer's type (SDAT). This sequence represents a PCR primer used for
CC detecting human APOC1 DNA polymorphisms
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCACCTTC 9
              ||||||||
Db          2 CCACCTTC 9
```

RESULT 169
ADC09948
ID ADC09948 standard; DNA; 10 BP.
XX
AC ADC09948;
XX
DT 18-DEC-2003 (first entry)
XX
DE Optical nucleic acid sensor molecule-related oligo, SEQ ID 360.
XX
KW Nucleic acid sensor molecule; ligase; cis-hammerhead; protein kinase; ds.
XX
OS Synthetic.
XX
PN WO2003014375-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025319.
XX
PR 09-AUG-2001; 2001US-0311378P.
PR 21-AUG-2001; 2001US-0313932P.
PR 13-SEP-2001; 2001US-00952680.
PR 13-NOV-2001; 2001US-0338186P.
PR 18-JAN-2002; 2002US-0349959P.
PR 13-MAR-2002; 2002US-0364486P.
PR 25-MAR-2002; 2002US-0367991P.
PR 04-APR-2002; 2002US-0369887P.
PR 01-MAY-2002; 2002US-0376744P.
PR 31-MAY-2002; 2002US-0385097P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N, Kurz M, Keefe T, Wilson C;
PI Grate D, Marshall KA, Mccauley T, Kurz J;
XX
DR WPI; 2003-300534/29.
XX
PT Nucleic acid sensor molecule, for identifying/detecting protein kinase in
PT a sample, comprises a target modulation domain which recognizes a target
PT molecule, a linker domain, a catalytic domain, and an optical signal
PT generator.
XX
PS Example 39; SEQ ID NO 360; 423pp; English.
XX
CC The present invention relates to nucleic acid sensor molecules (I), which
CC comprise a target modulation domain that recognizes a target molecule
CC (TM), a linker domain, a catalytic domain, and an optical signal
CC generating unit. The catalytic domain comprises a ligase or cis-
CC hammerhead. (I) are useful for identifying or detecting TM in a sample,
CC preferably a protein kinase in a sample. Target molecules include
CC proteins, post-translationally modified forms of proteins, peptides,
CC nucleic acids, oligosaccharides, nucleotides, metabolites, drugs, toxins,
CC biohazards, ions, carbohydrates, polysaccharides, hormones, receptors,
CC antigens, antibodies, viruses, metabolites, co-factors, drugs, dyes,
CC nutrients, growth factors, cCMP, cAMP or cGMP, protein kinase,
CC phosphorylated protein kinase, extracellular signal regulated kinase
CC (ERK), a component or product of mitogen activated protein (MAP) kinase
CC pathway, a MAP kinase pathway associated protein, an extracellular
CC component of MAP kinase pathway, a component of ERK1/2 MAP, JNK MAP or
CC P38 MAP kinase pathway, an endogenous form of MAP kinase (MEK), MAP
CC kinase kinase, or MAP kinase (MEKKK), or RAF kinase, Ras protein,
CC phosphatase, GTP binding protein, G-protein coupled receptor (GPCR),
CC cytokine, growth factor, cellular metabolite, small molecule or lysozyme.
CC (I) are also useful for identifying a modulator of protein kinase
CC activity. The present sequence was used to illustrate the invention.
XX
SQ Sequence 10 BP; 0 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCTTGGG 14
              ||||||||
Db          2 TTCTTGGG 9
```

RESULT 170
AAL62417/c
ID AAL62417 standard; DNA; 20 BP.
XX
AC AAL62417;
XX

```
DT   06-OCT-2003  (first entry)
XX
DE   Human ABC transporter MHC I antisense oligonucleotide, ISIS 206598.
XX
KW   ABC transporter; ABCT; major histocompatibility complex; MHC; cytostatic;
KW   hyperproliferative; autoimmune disorder; antisense gene therapy;
KW   inflammation; tumour formation; immunosuppressive; antimicrobial; human;
KW   phosphorothioate backbone; antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051309-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040101.
XX
PR   17-DEC-2001; 2001US-00024369.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Ward DT,  Freier SM;
XX
DR   WPI; 2003-577305/54.
XX
PT   New antisense compound that hybridizes and inhibits the nucleic acid
PT   encoding ABC transporter major histocompatibility complex 1, for treating
PT   diseases or conditions such as a hyperproliferative or autoimmune
PT   disorder.
XX
PS   Claim 3; Page 81; 112pp; English.
XX
CC   The invention relates to a compound targetted to a nucleic acid molecule
CC   encoding ABC transporter (ABCT) major histocompatibility complex (MHC) 1
CC   where the compound specifically hybridises with the nucleic acid molecule
CC   and inhibits expression of ATM or specifically hybridises with at least a
CC   portion of an active site on the nucleic acid molecule. The invention is
CC   useful for inhibiting the expression of ATM in cells or tissues. The
CC   invention is useful for treating an animal with hyperproliferative or
CC   autoimmune disorder. The invention is useful for diagnostics,
CC   therapeutics, prophylaxis, as research reagents and kits, for
CC   distinguishing functions of various members of a biological pathway and
CC   in antisense gene therapy. The invention is also useful prophylactically
CC   e.g., to prevent or delay infection, inflammation or tumour formation.
CC   The present sequence is an antisense oligo targetted to human ABC
CC   transporter MHC I DNA. This sequence is used to illustrate the method of
CC   the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match            35.0%;  Score 7;  DB 1;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 CTTCTTGGGCAGAAG 20
              |||||     |||||
Db         20 CTTCTGCCCAAGAAG 6


RESULT 171
ABH88612/c
ID   ABH88612 standard; DNA; 12 BP.
XX
AC   ABH88612;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 288605 for detecting SNP TSC0013593.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 288605; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match            32.0%;  Score 6.4;  DB 1;  Length 12;
  Best Local Similarity   87.5%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GGCAGAAG 20
              || |||||
Db         11 GGAAGAAG 4


RESULT 172
ABH88613/c
ID   ABH88613 standard; DNA; 12 BP.
XX
AC   ABH88613;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 288606 for detecting SNP TSC0013593.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 288606; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 32.0%; Score 6.4; DB 1; Length 12;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GGCAGAAG 20
|| |||||
Db 11 GGAAGAAG 4

RESULT 173
AAZ79378
ID AAZ79378 standard; DNA; 10 BP.
XX
AC AAZ79378;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1806.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 116; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for